

5914

347  
344  
350

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FIGURE 1E

SEQUENCE	CGACATCCGCGCGGCTCCAGCAGGAGGCTGCTTCCGCGCTGCGCGCGGCGGCGGCTTCAAGCTCAACTCCGCGGAG	
1464	CC	
1465	GC	
1466	AG	
1467	G	
1468	T	
1469	G	
1470		
SEQUENCE	CAGCTCGAAAGGGTGGTCTTTGACGAGGCTXGGGCTTCCGCGCATCGGCAAGCGGAGAGACXGGCAAGC	
1534	C	
1535	CC	
1536	GC	
1537	TA	
1538	TA	
1539	TA	
1540	TA	
1541	TA	
1542	TA	
1543	TA	
1544	TA	
1545	TA	
1546	TA	
1547	TA	
1548	TA	
1549	TA	
1550	TA	
1551	TA	
1552	TA	
1553	TA	
1554	TA	
1555	TA	
1556	TA	
1557	TA	
1558	TA	
1559	TA	
1560	TA	
1561	TA	
1562	TA	
1563	TA	
1564	TA	
1565	TA	
1566	TA	
1567	TA	
1568	TA	
1569	TA	
1570	TA	
1571	TA	
1572	TA	
1573	TA	
1574	TA	
1575	TA	
1576	TA	
1577	TA	
1578	TA	
1579	TA	
1580	TA	
1581	TA	
1582	TA	
1583	TA	
1584	TA	
1585	TA	
1586	TA	
1587	TA	
1588	TA	
1589	TA	
1590	TA	
1591	TA	
1592	TA	
1593	TA	
1594	TA	
1595	TA	
1596	TA	
1597	TA	
1598	TA	
1599	TA	
1600	TA	
1601	TA	
1602	TA	
1603	TA	
1604	TA	
1605	TA	
1606	TA	
1607	TA	
1608	TA	
1609	TA	
1610	TA	
1611	TA	
1612	TA	
1613	TA	
1614	TA	
1615	TA	
1616	TA	
1617	TA	
1618	TA	
1619	TA	
1620	TA	
1621	TA	
1622	TA	
1623	TA	
1624	TA	
1625	TA	
1626	TA	
1627	TA	
1628	TA	
1629	TA	
1630	TA	
1631	TA	
1632	TA	
1633	TA	
1634	TA	
1635	TA	
1636	TA	
1637	TA	
1638	TA	
1639	TA	
1640	TA	
1641	TA	
1642	TA	
1643	TA	
1644	TA	
1645	TA	
1646	TA	
1647	TA	
1648	TA	
1649	TA	
1650	TA	
1651	TA	
1652	TA	
1653	TA	
1654	TA	
1655	TA	
1656	TA	
1657	TA	
1658	TA	
1659	TA	
1660	TA	
1661	TA	
1662	TA	
1663	TA	
1664	TA	
1665	TA	
1666	TA	
1667	TA	
1668	TA	
1669	TA	
1670	TA	
1671	TA	
1672	TA	
1673	TA	
1674	TA	
1675	TA	
1676	TA	
1677	TA	
1678	TA	
1679	TA	
1680	TA	
1681	TA	
1682	TA	
1683	TA	
1684	TA	
1685	TA	
1686	TA	
1687	TA	
1688	TA	
1689	TA	
1690	TA	
1691	TA	
1692	TA	
1693	TA	
1694	TA	
1695	TA	
1696	TA	
1697	TA	
1698	TA	
1699	TA	
1700	TA	
1701	TA	
1702	TA	
1703	TA	
1704	TA	
1705	TA	
1706	TA	
1707	TA	
1708	TA	
1709	TA	
1710	TA	
1711	TA	
1712	TA	
1713	TA	
1714	TA	
1715	TA	
1716	TA	
1717	TA	
1718	TA	
1719	TA	
1720	TA	
1721	TA	
1722	TA	
1723	TA	
1724	TA	
1725	TA	
1726	TA	
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1728	TA	
1729	TA	
1730	TA	
1731	TA	
1732	TA	
1733	TA	
1734	TA	
1735	TA	
1736	TA	
1737	TA	
1738	TA	
1739	TA	
1740	TA	
1741	TA	
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1743	TA	
1744	TA	
1745	TA	
1746	TA	
1747	TA	
1748	TA	
1749	TA	
1750	TA	

**FIGURE 1F**

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CCCTGGAGGTCGACGGTGGGGATCGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

# FIGURE 1H

CCCTGGAGGTCGACGGTGGGGATCGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

CCCTGGAGGTCGACGGTGGGGATCGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

CCCTGGAGGTCGACGGTGGGGATCGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

CCCTGGAGGTCGACGGTGGGGATCGGGGAGGAGCTGGCTCTCCGCCAAGGAGTAG

2499

2498

2503



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WENALPLFEPKQAVLLVDGHHLAYRTFFALKGLTTSRQEPVOAVYGFAXSLLKALKEOG	DAUVVVVFQAK		
GG	H	I	69
E	V	V	68
	Y	K	70
APSPRHEAYEAYKAGRAPTEOFPROLALIKELVOLLGLXRLEVPOYEADUVALTAKKAEKEGYEVRI			
GG	A	S	139
	V	R	138
	F		140
	FT		
INOROLYOLLSORIAVLHPEGYLITPAWLWEKYGLRPEOWVQYRALXGDPSONHPCVKGICENTAXKLLX			
K	H	D	209
E	Y	A	208
V	H	F	210
	E	V	
EWOSLEHLKHLQAVKPPXXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXAREPOREGLRAFLELEF			
A	AI	D	278
	K	WO	
FOH	SL	O	277
	Q	A	
	ENV	R	280
	K	L	
	R	LE	
	L	OC	
GSLLHEFCOLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMVAELLALAAARXGAVHRAOXDPLXGLROLKEV			
S	K	D	348
G	L	SF	347
A	A	C	350
	AP	K	
		C	
		D	
		WE	
		L	
		O	
		R	
		A	
		A	
		K	

591/01

[illegible]

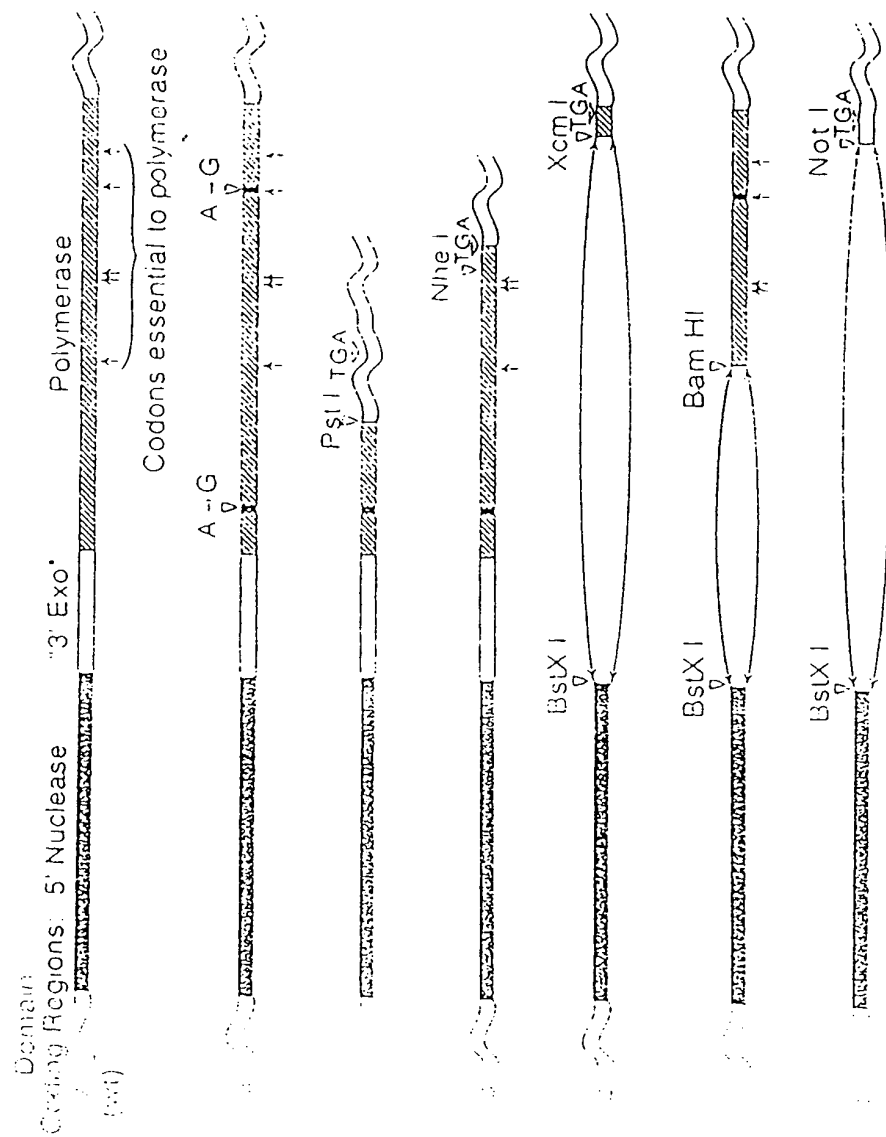
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# FIGURE 2C

SEQUENCE	SFPKURAWI EKILEGRRRCYVETLFCRRRYVPOLHARVKSUREAERMAFHMPVOCTAADLHKLRMMVKL	
768	.....E.....	768
769	Y.....G.....	767
770	.....K.....	770
SEQUENCE	EPRLXEMGARMILLOVHDELVLLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
833	.....E.....A.....R.....	833
834	.....O.....L.....D.....R.....W.....O.....	831
835	.....R.....L.....OA.....E.....A.....KA.....C.....	835

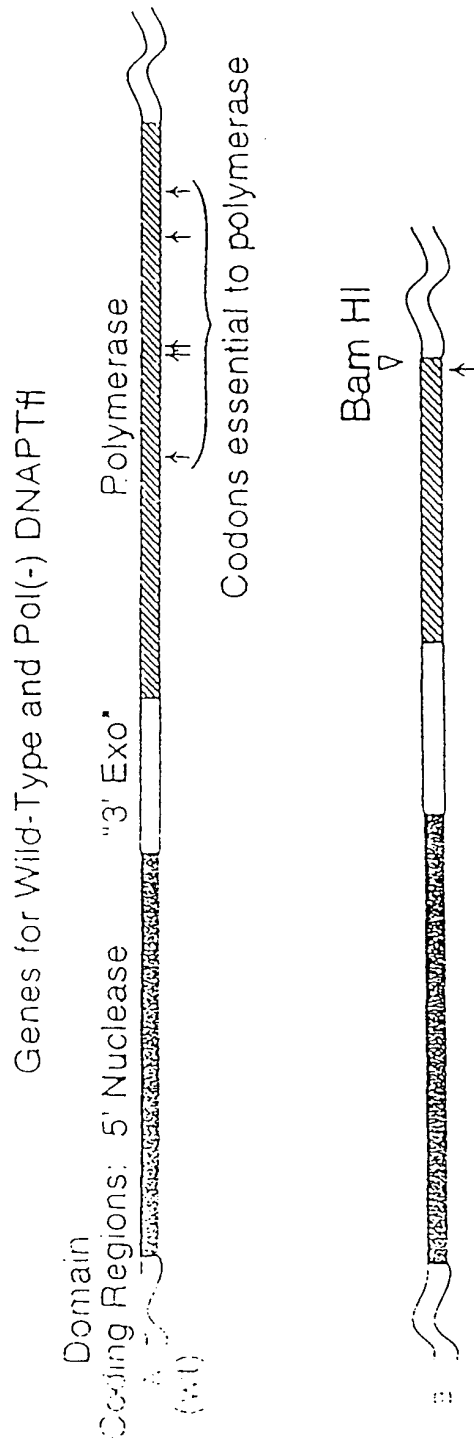
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FIGURE 3



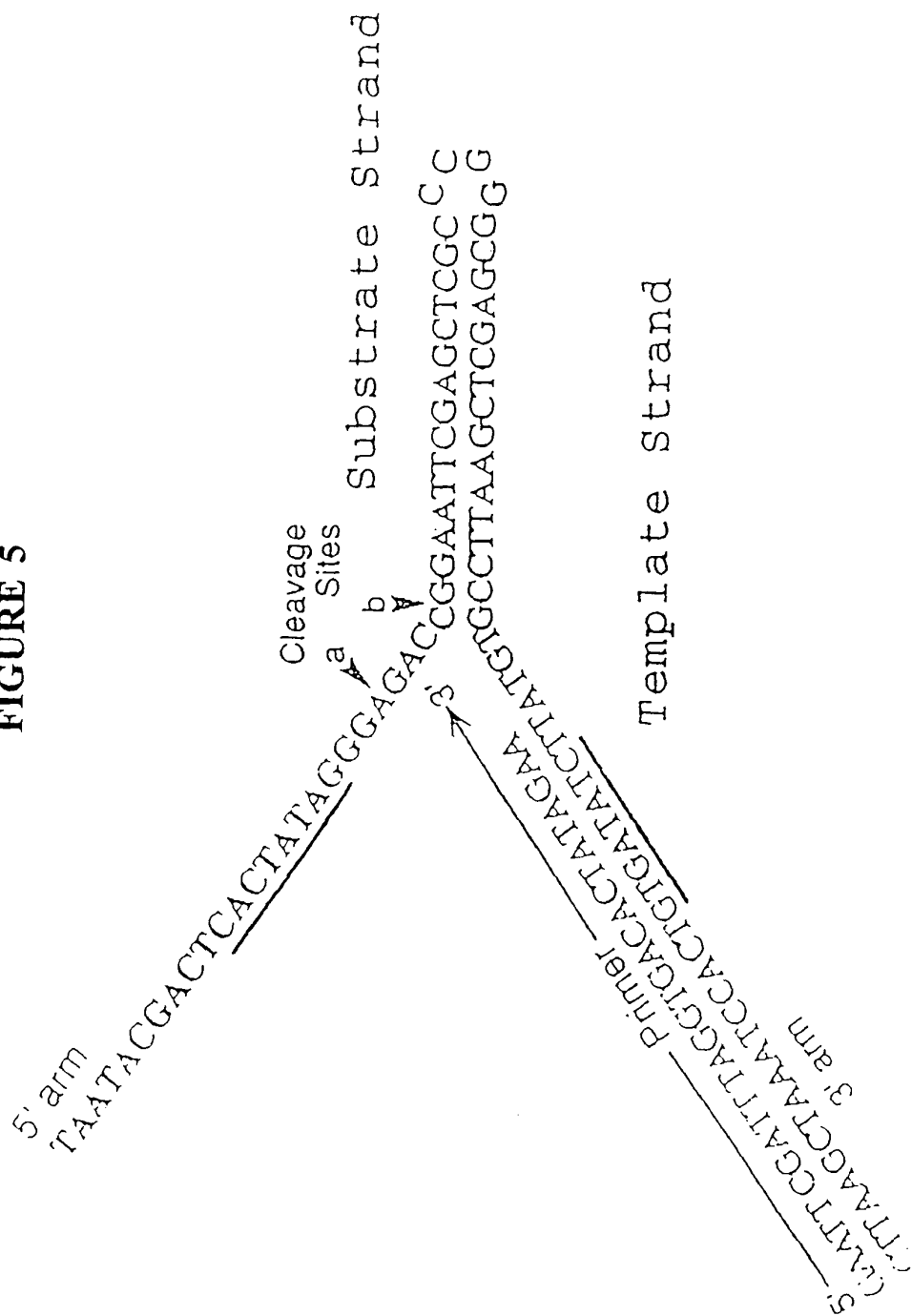
13/16s

FIGURE 4



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FIGURE 5



DNAP  
TARGET  
DNA

T			S		
M	-	+	-	+	M

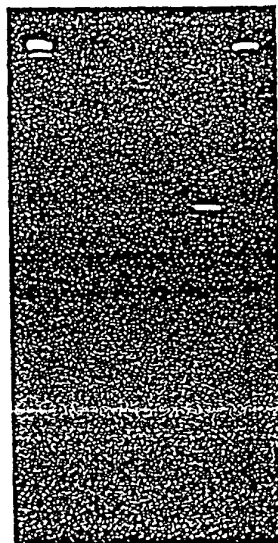


FIGURE 6

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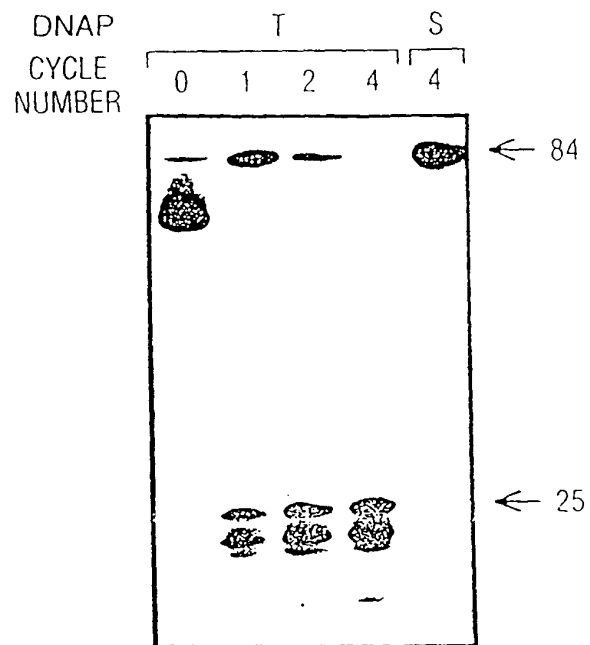


FIGURE 7

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	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

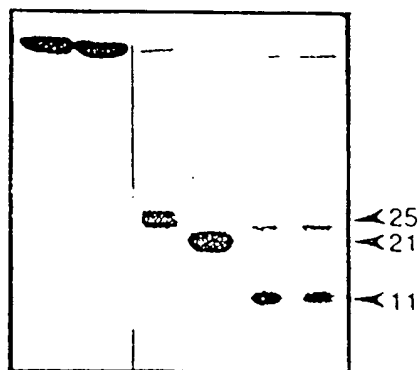


FIGURE 8A

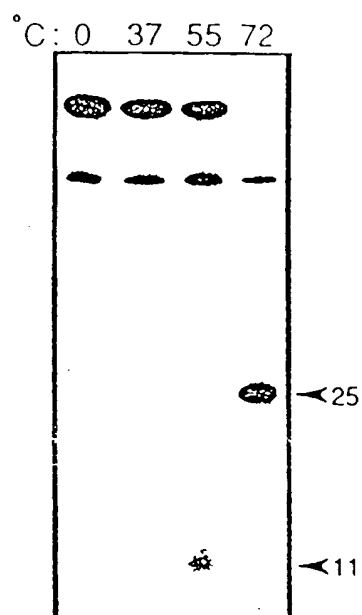


FIGURE 8B

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18/165

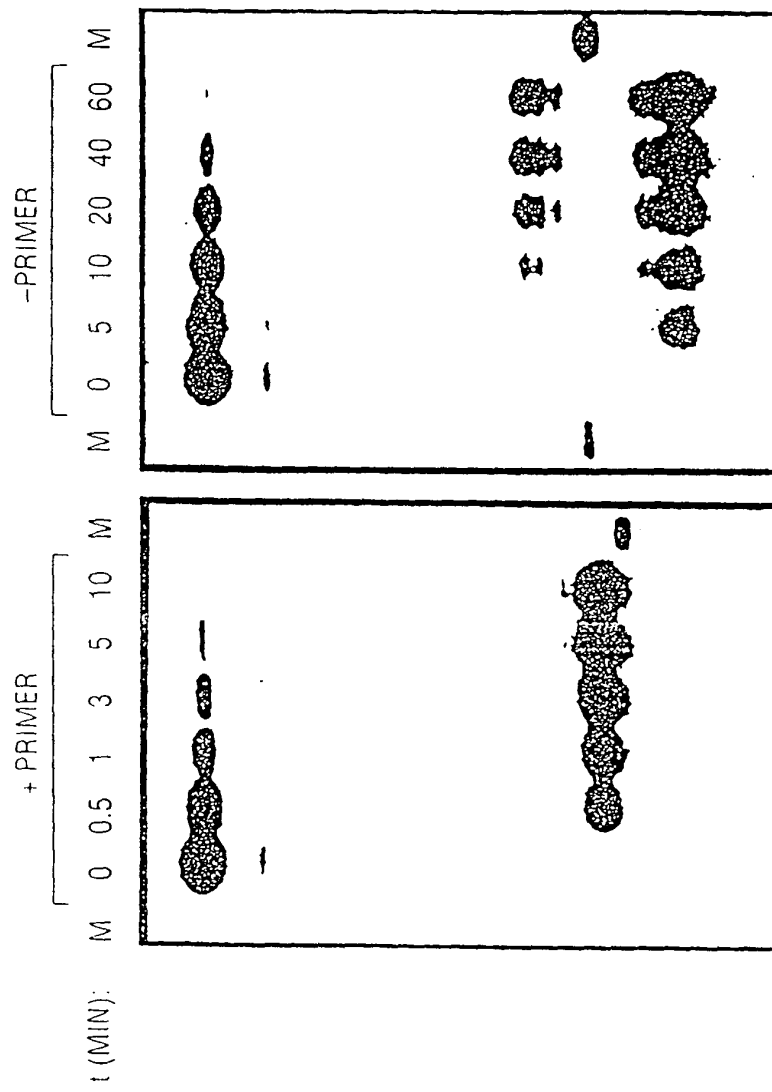
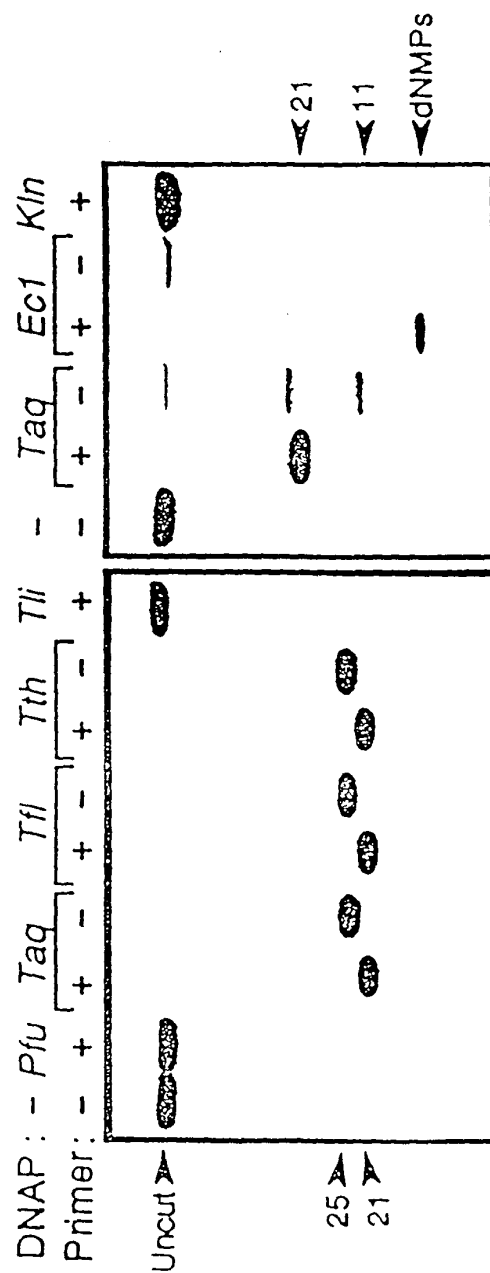


FIGURE 9A

FIGURE 9B

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**FIGURE 10B**

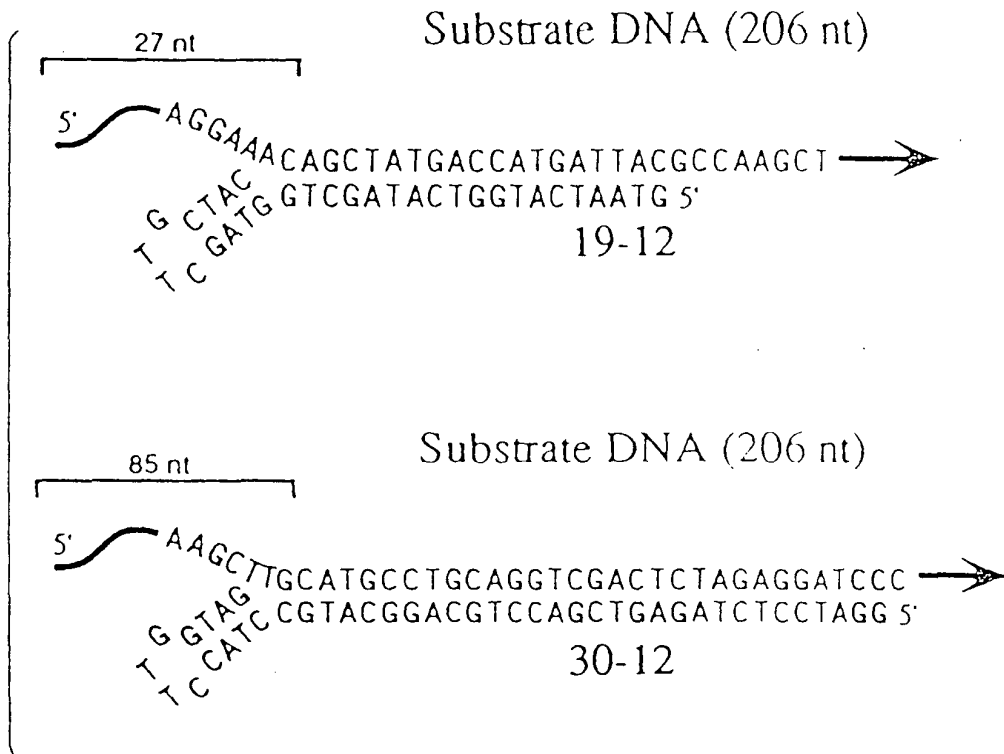


FIGURE 11A

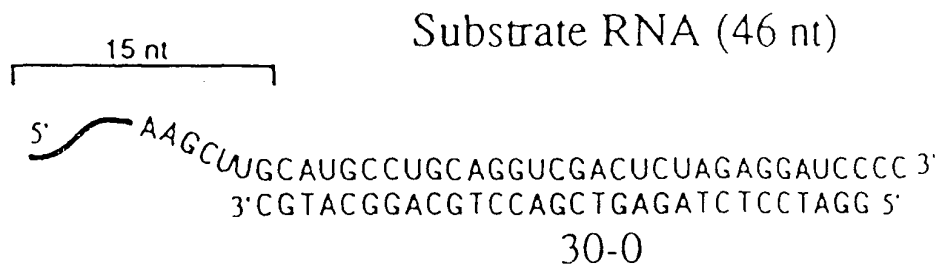


FIGURE 12A

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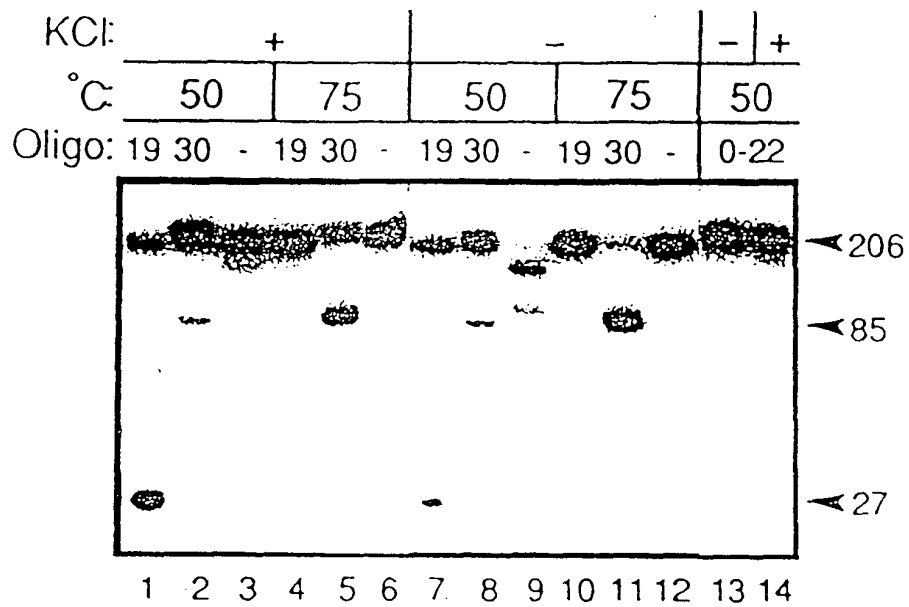


FIGURE 11B

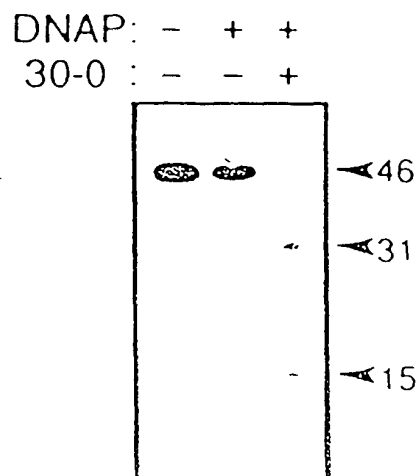
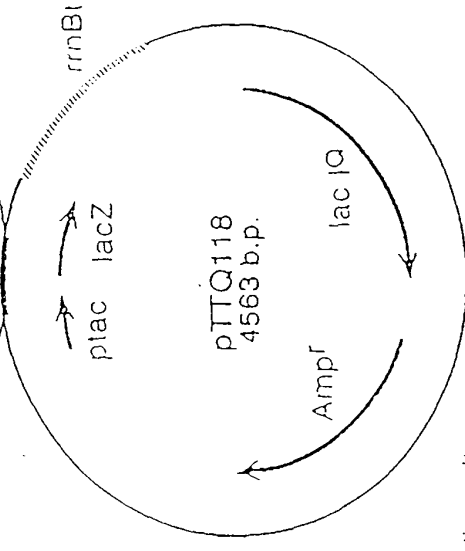
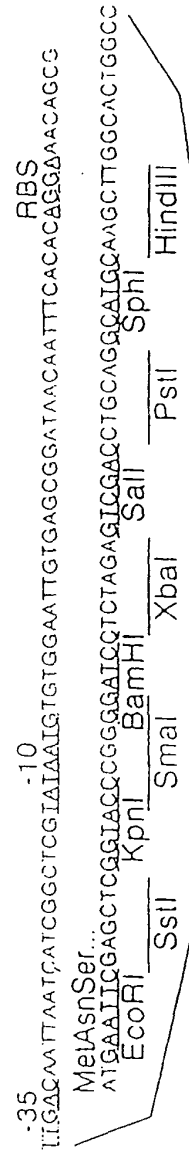


FIGURE 12B

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FIGURE 13

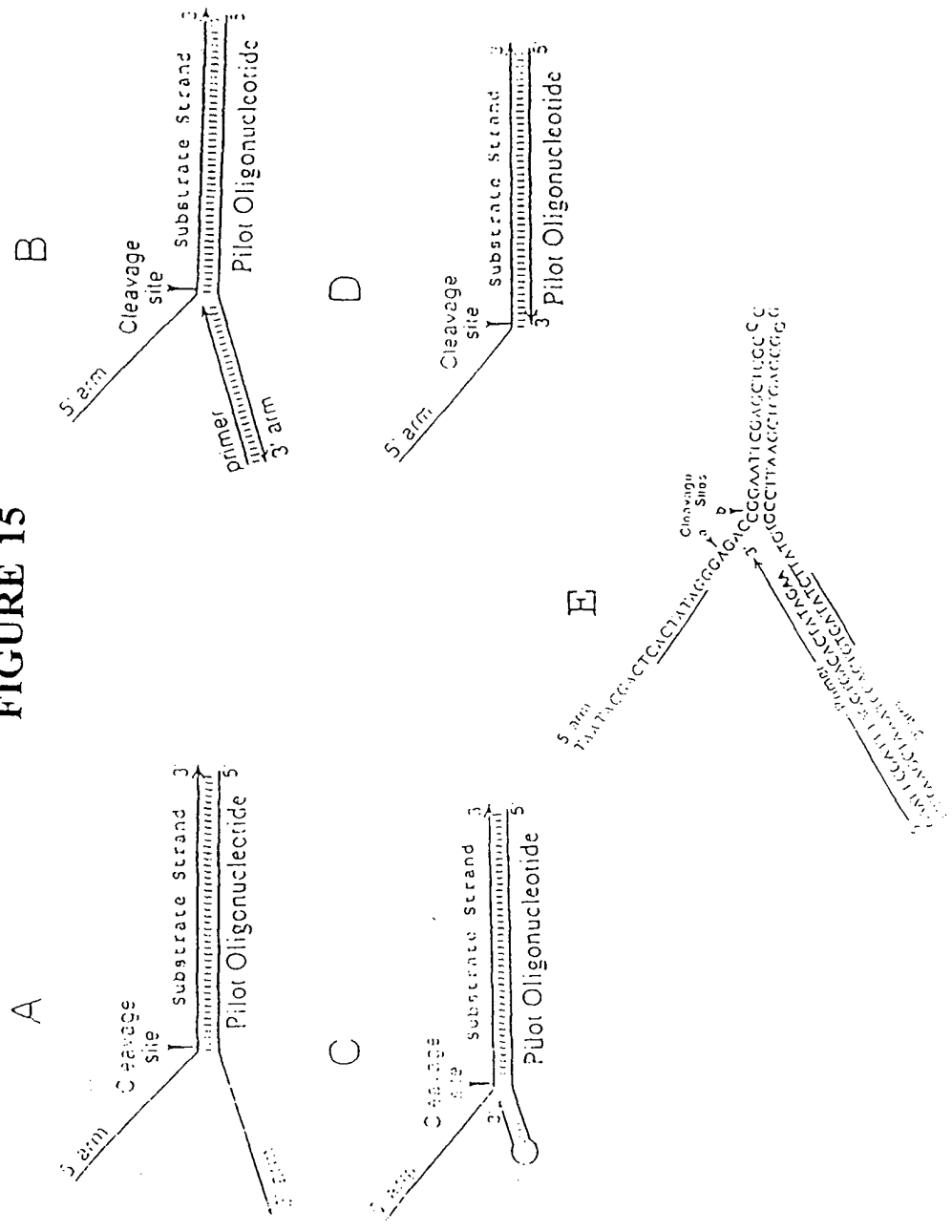


RBS: Ribosome binding site  
 plac: Synthetic tac promoter  
 lacIQ: Lac repressor gene  
 lacZ: Beta-galactosidase alpha fragment  
 rrnBt: E. coli rrnB transcription terminator



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FIGURE 15





5/1/5e

66347-70347

1 2 3 4 5 6 7

UNCLEAVED SUBSTRATE

CLEAVED SUBSTRATE

-	-	-	+	-	-	+	dNTPs
-	-	+	+	-	-	+	PRIMER
Taq	4e			5b			ENZYME

FIGURE 16

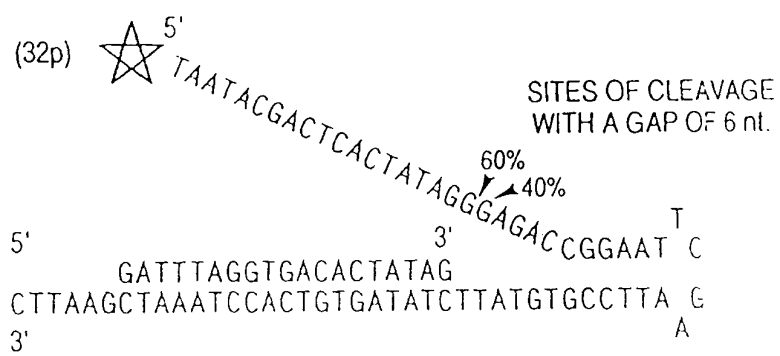
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ENZYME	Taq	-	Taq	4b	4c	4d	4e	4f
PRIMED M13	-	+	+	+	+	+	+	+

FIGURE 17



**FIGURE 18A**

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	"4d"				"4b"		UNMODIFIED	
	NO POL. ACTIVITY				2 PT. MUTATION SMALL ACTIVITY		DNAP Taq	
1	2	3	4		5	6	7	8
-	-	-	+	+	-	+	-	+

dNTP

34 NUC. —————

← HAIRPIN TEST MODULE

← CONVERSION TO DOUBLE STRANDED (COMPLETE EXTENSION OF PRIMER)

DESIRED PRODUCT 21 NUC. —————

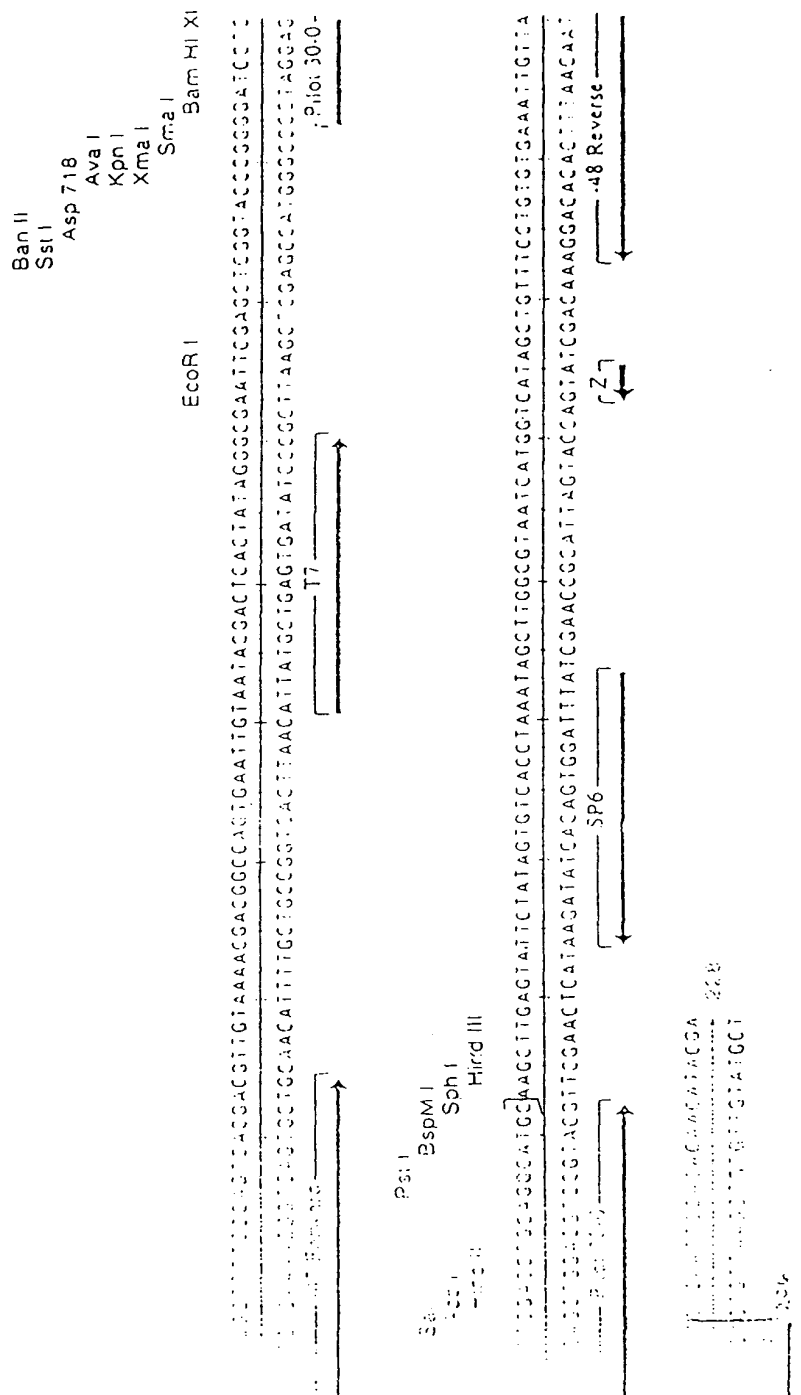
MULTIPLE BANDS CAUSED BY POLYMERIZATION

↑ SOME ABERRANT CLEAVAGE WITH "4b" BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

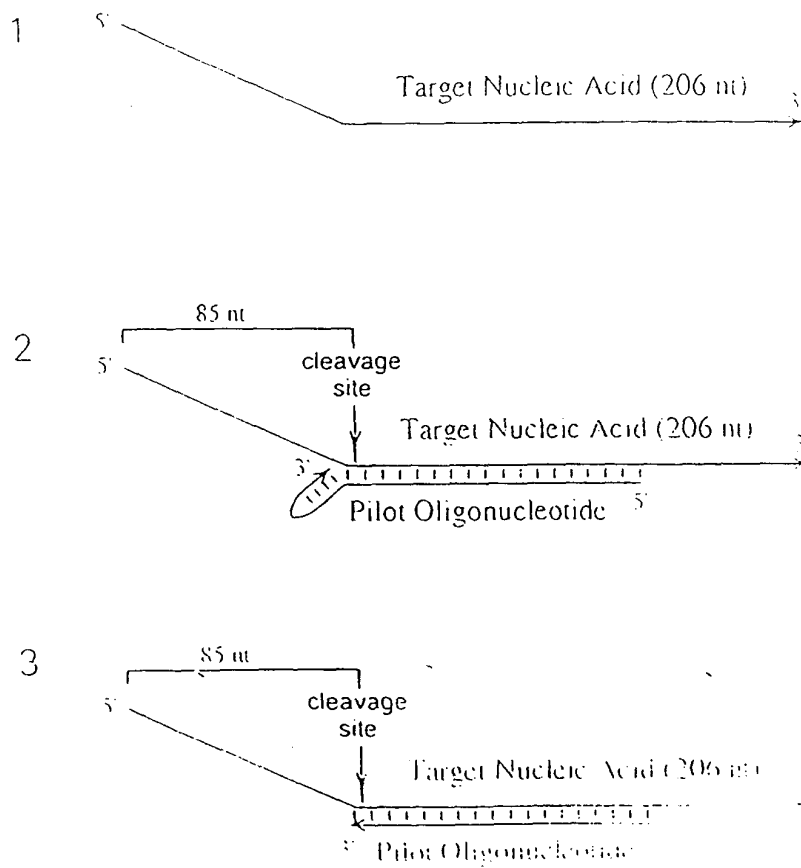
FIGURE 18B

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FIGURE 19



**FIGURE 20A**



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CONFIDENTIAL

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I			II			III			IV			V			I			VI		
1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3

206 —  — 206

85 —  — 85

FIGURE 20B

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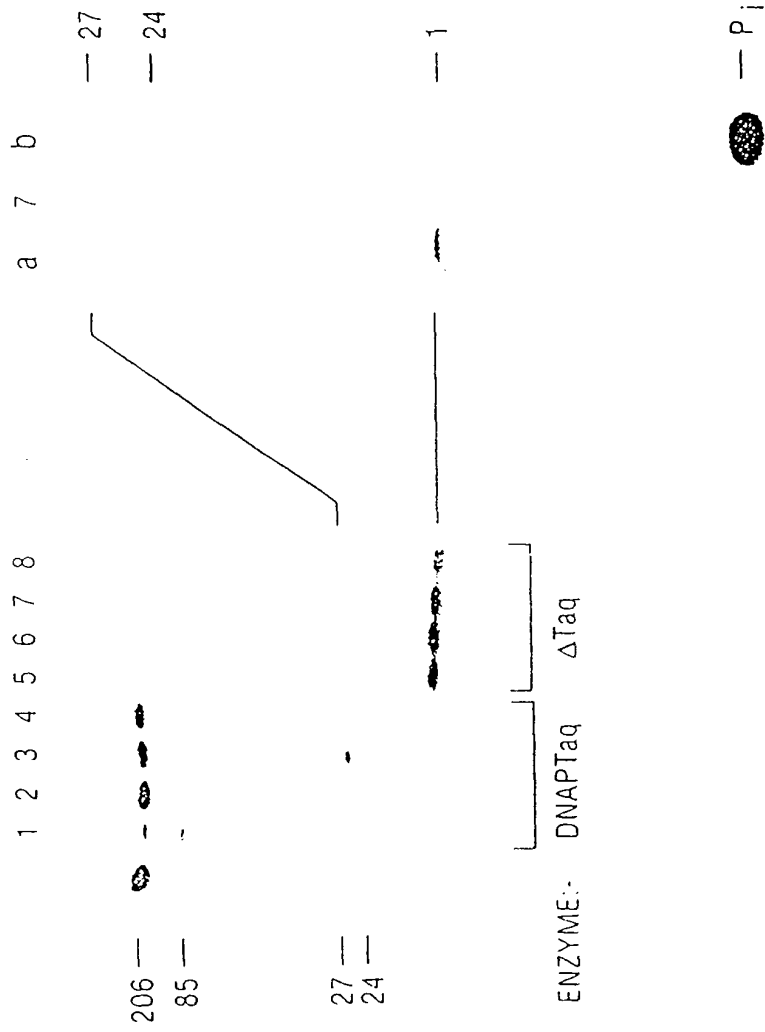


FIGURE 21A

FIGURE 21B



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FIGURE 22A

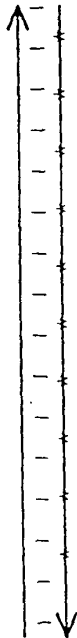
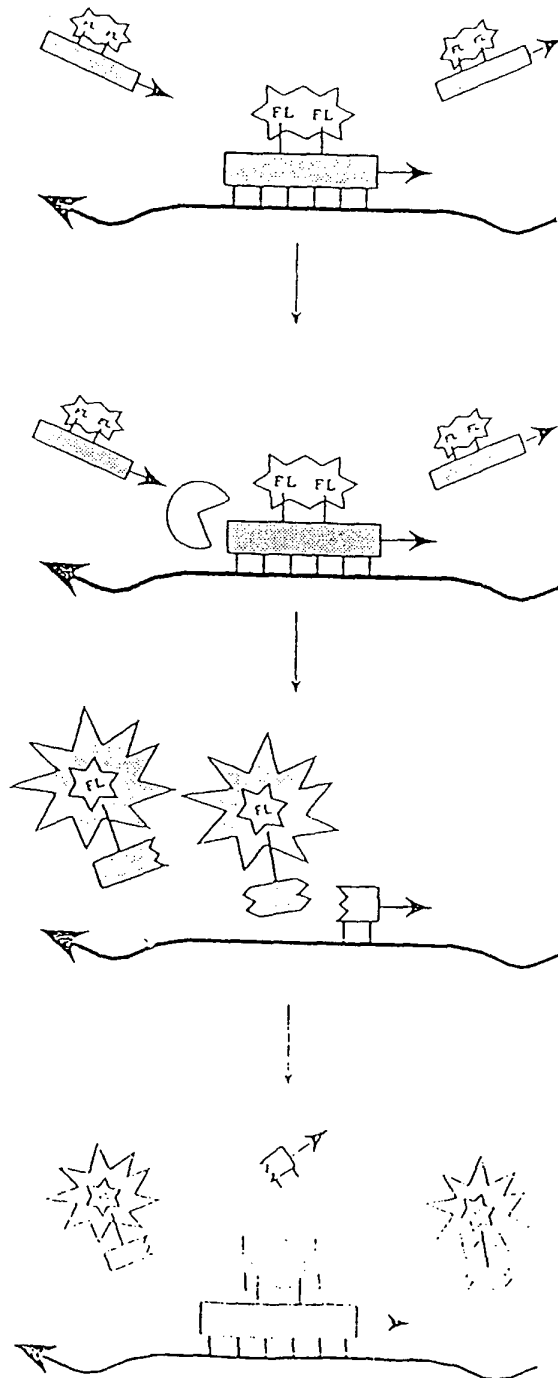


FIGURE 22B

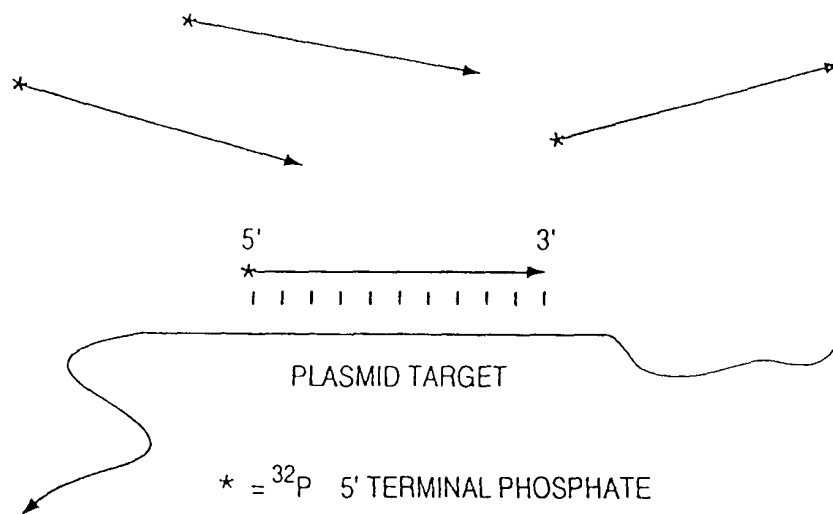
\* = 32p



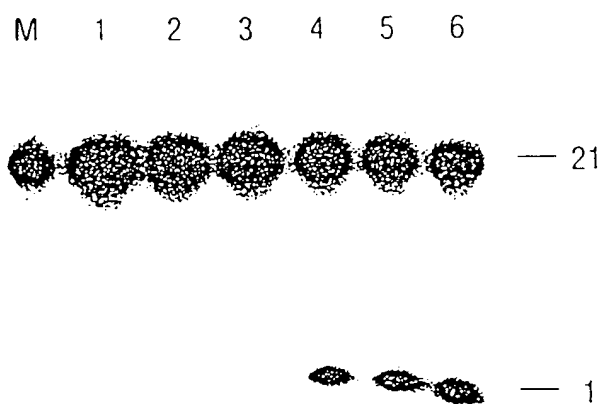
FIGURE 23



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**FIGURE 24A**



**FIGURE 24B**

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FIGURE 25

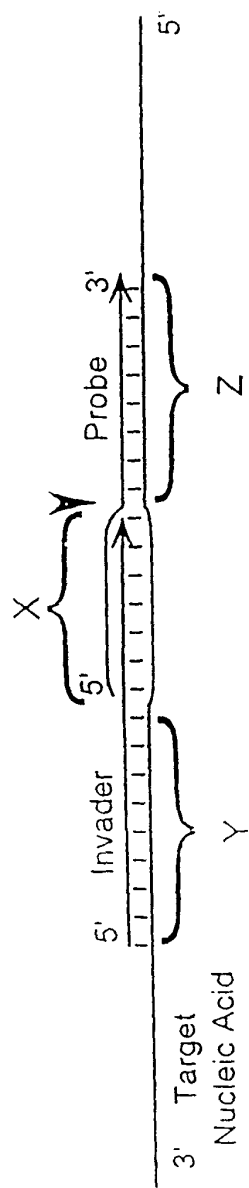
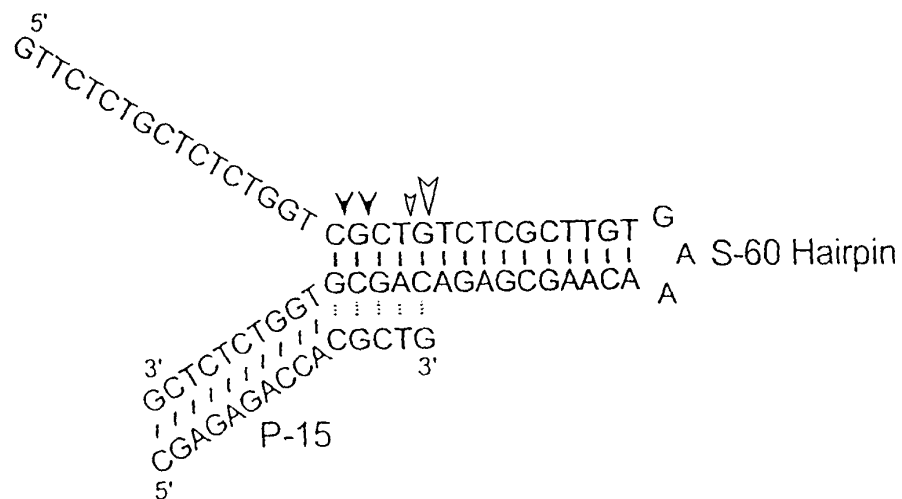


FIGURE 26



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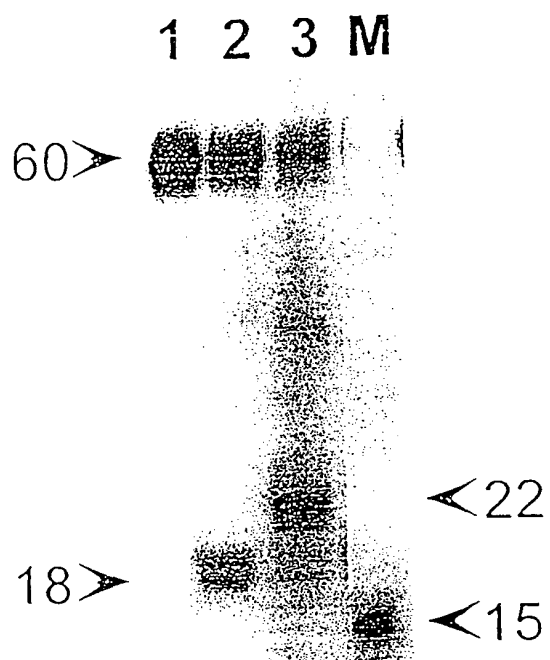
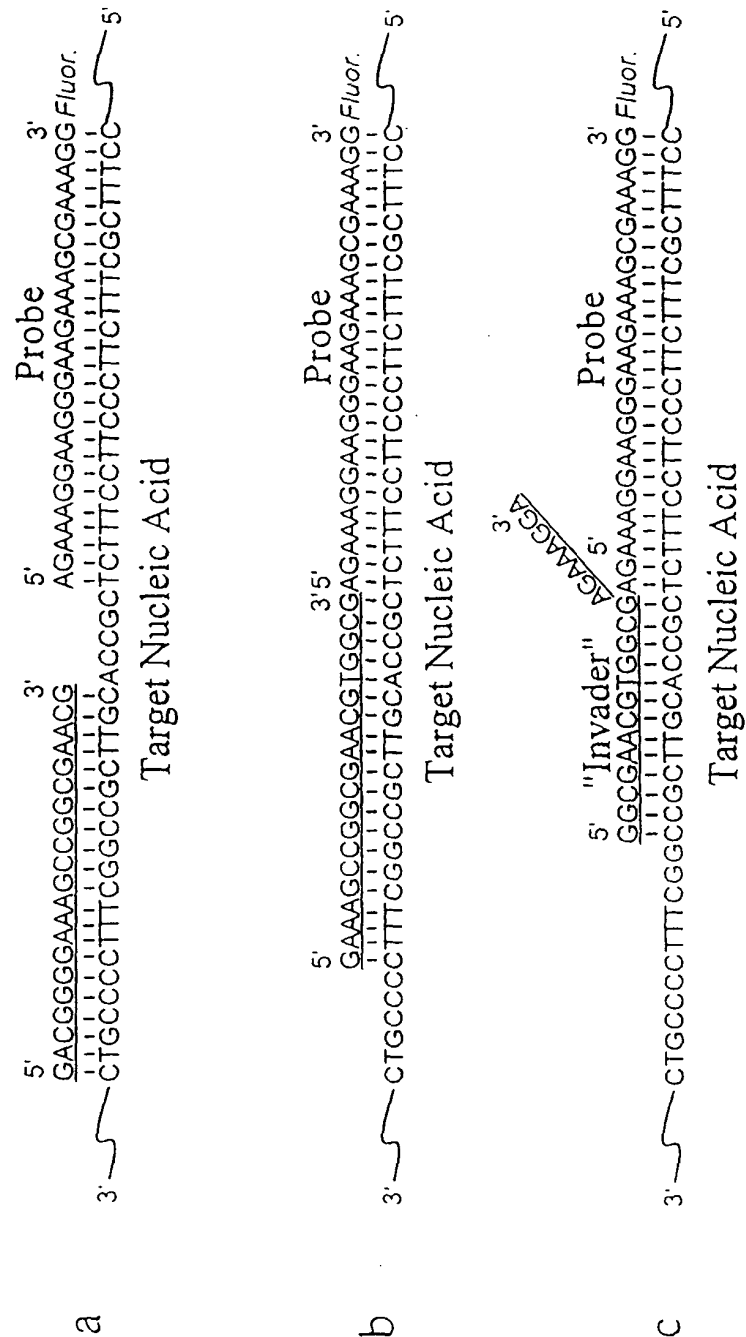


FIGURE 27

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FIGURE 28

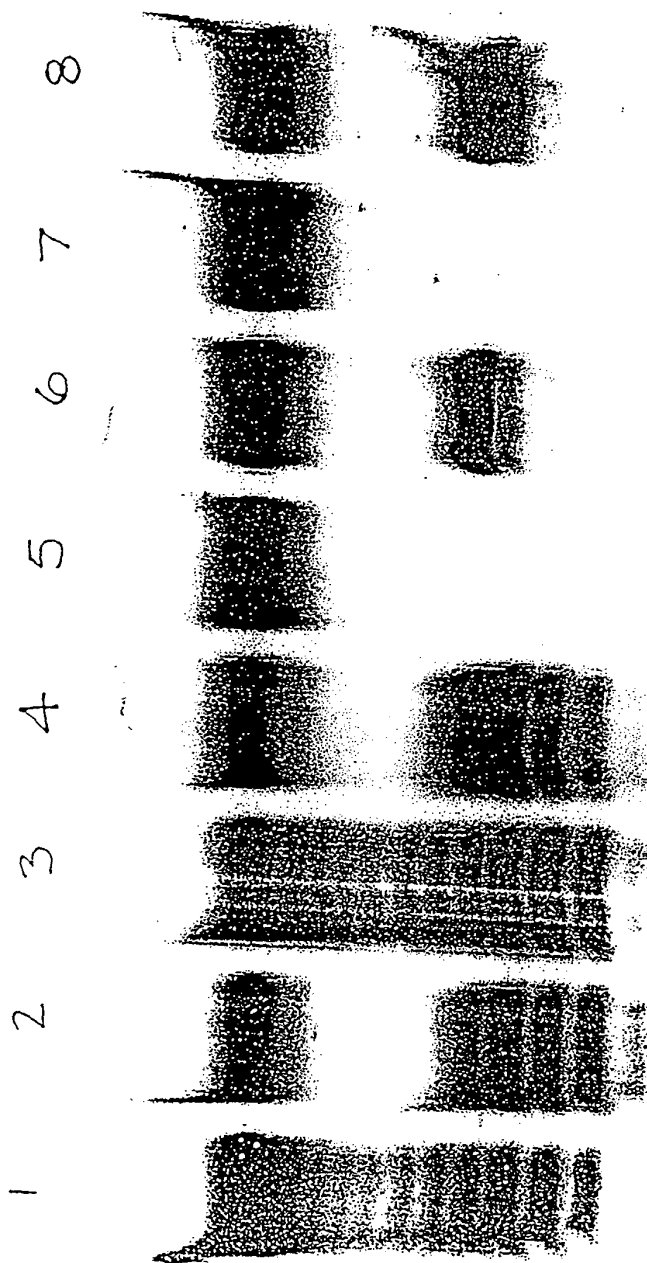




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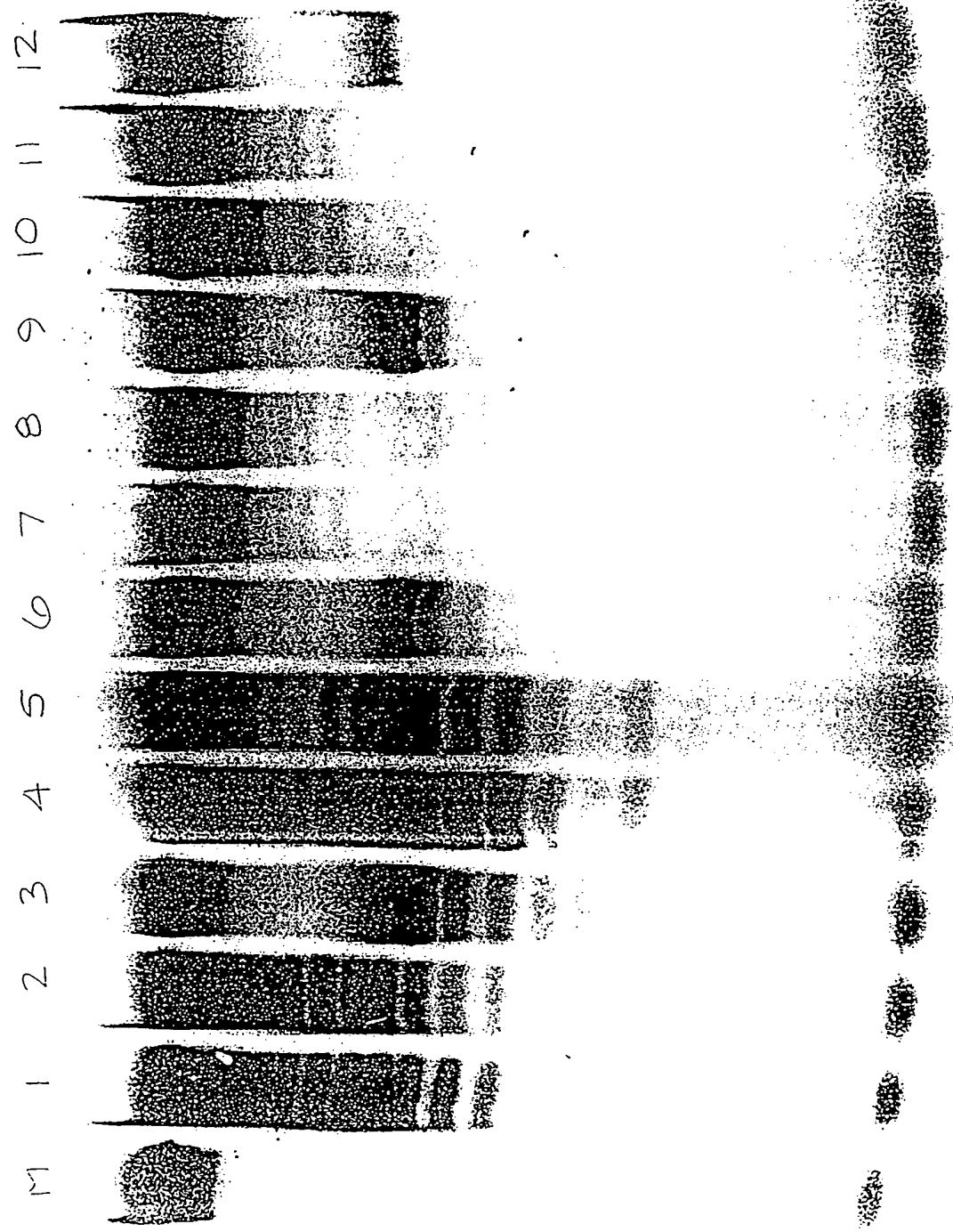
CONFIDENTIAL

FIGURE 29



26A

FIGURE 30

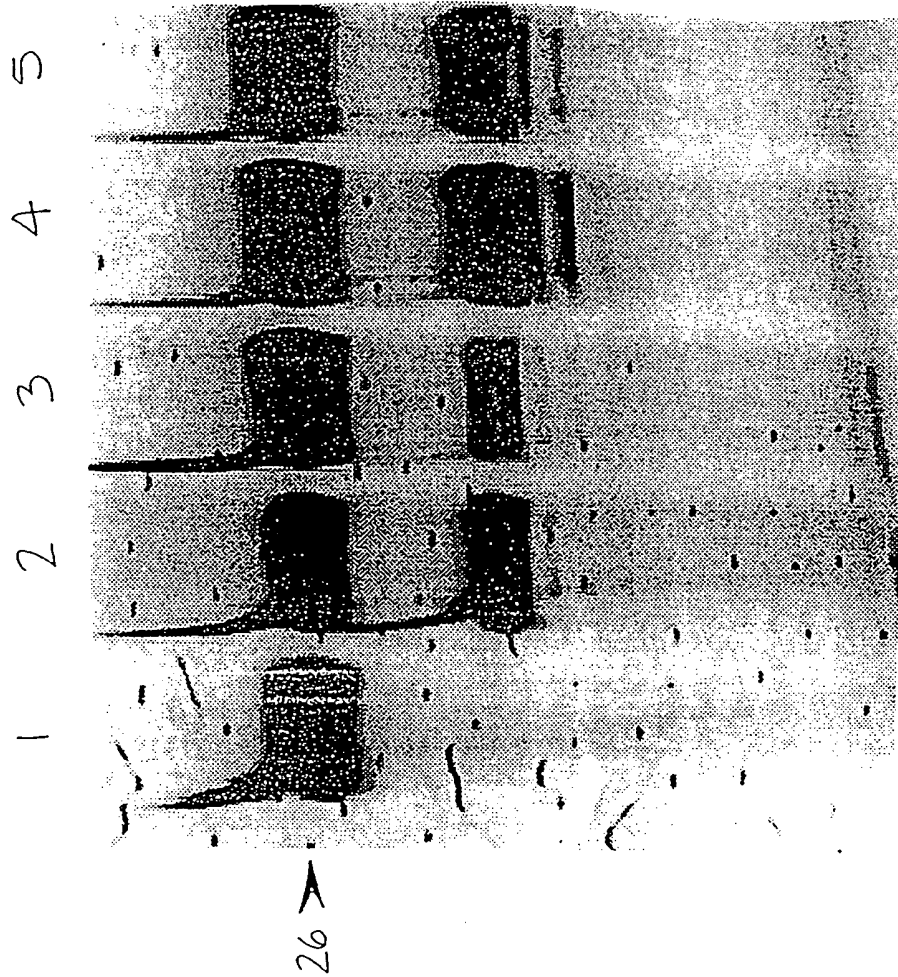


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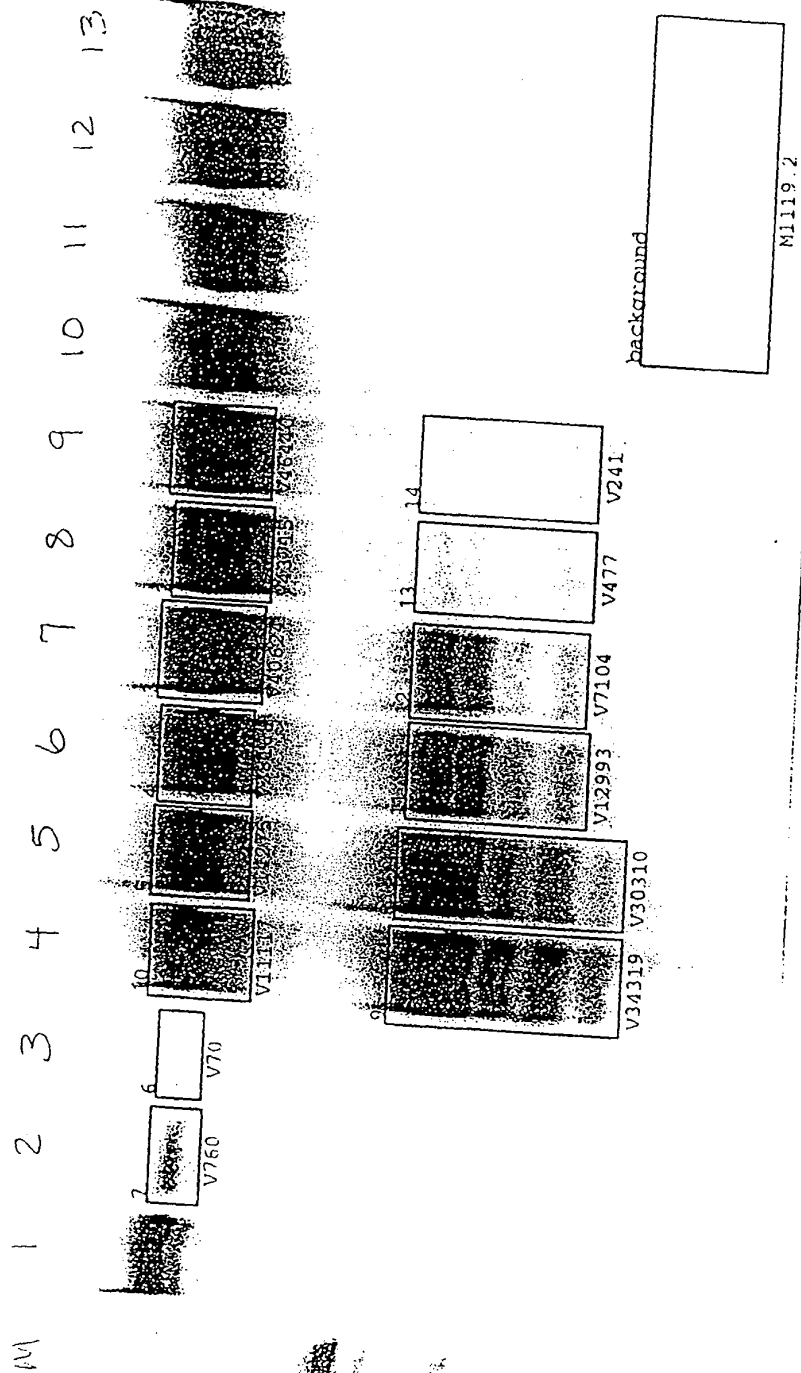
00577-0366

FIGURE 31



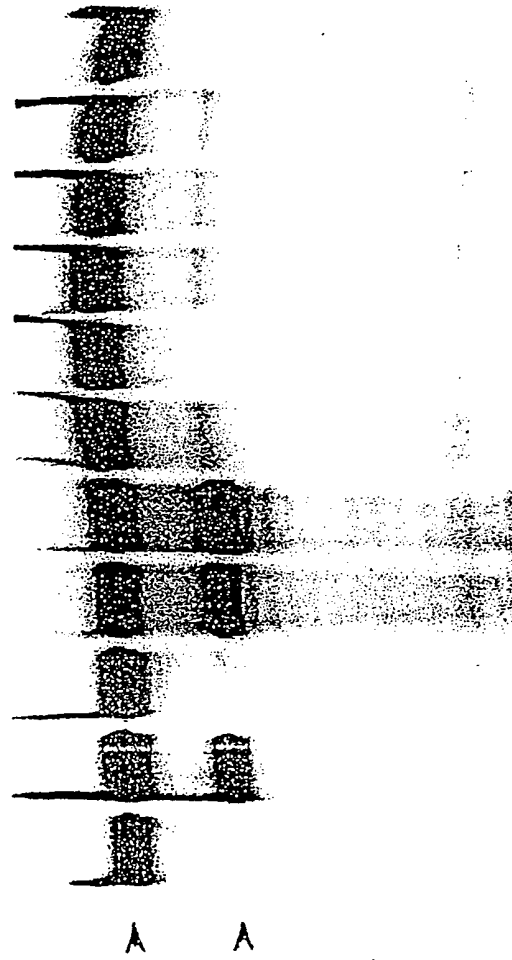
-59/1/hh

FIGURE 32



591/5A

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11



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DATE RECEIVED

FIGURE 34

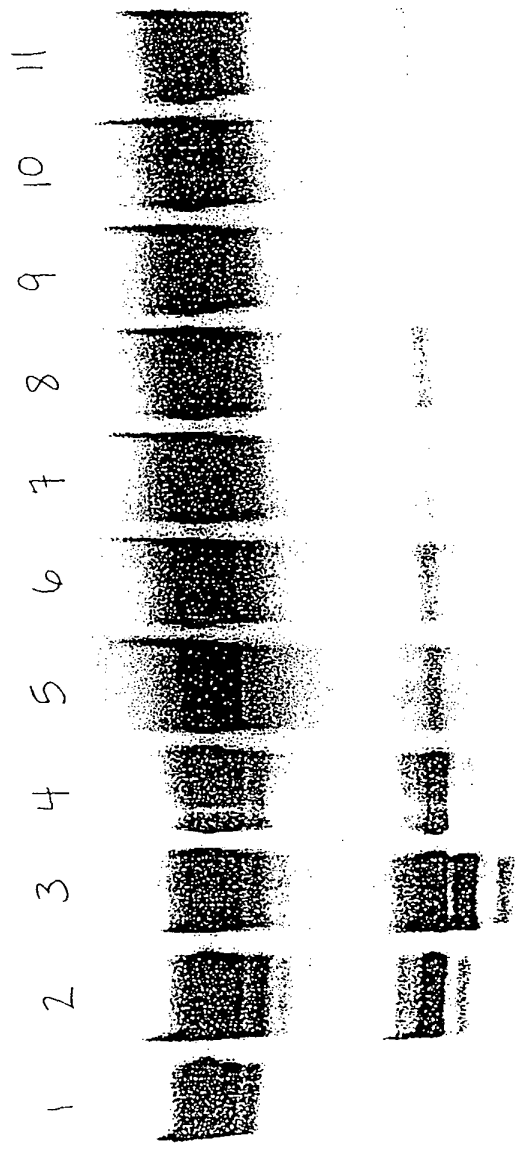
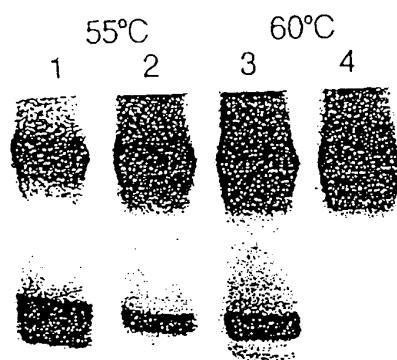


FIGURE 35



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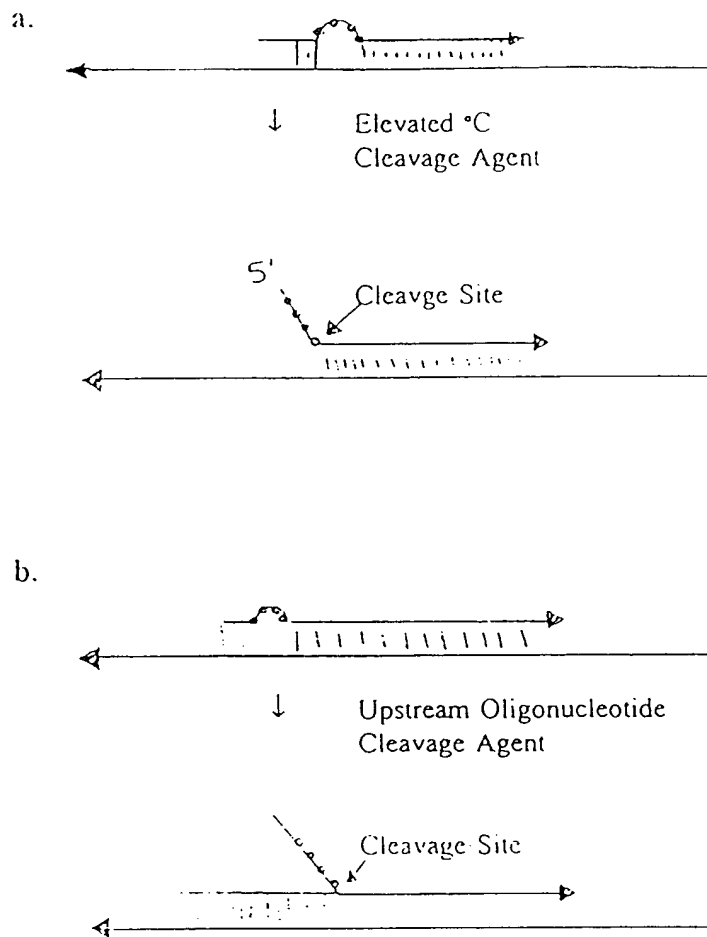


FIGURE 36

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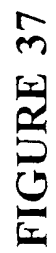
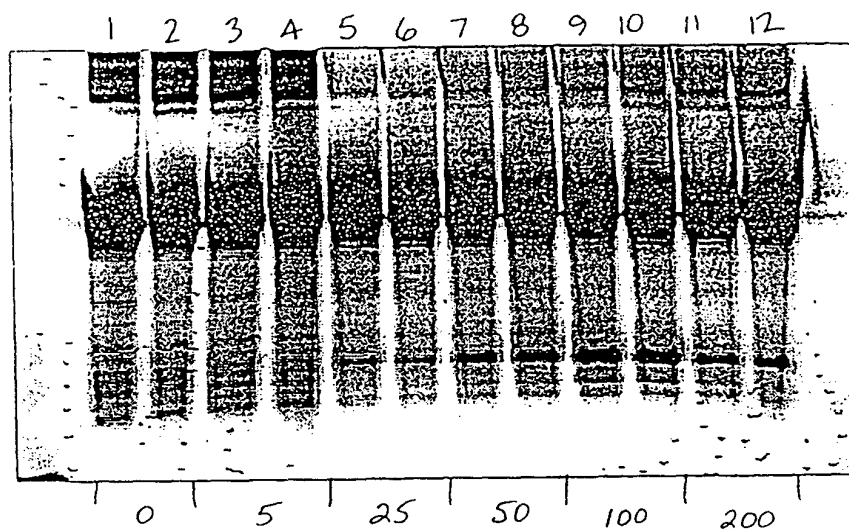


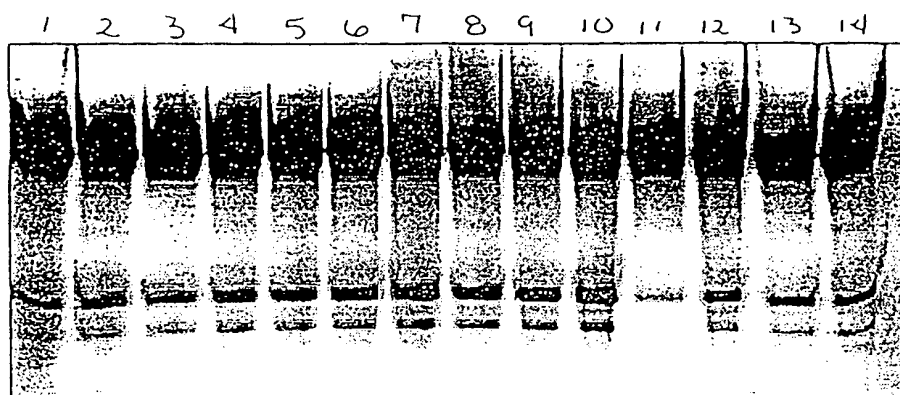
FIGURE 37

FIGURE 38



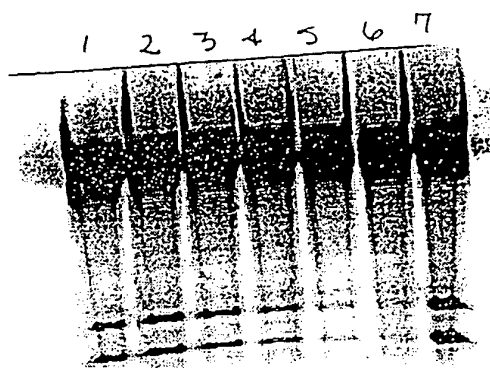
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FIGURE 39



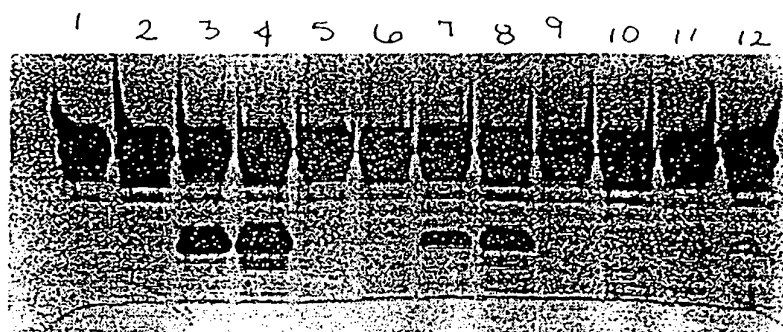
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FIGURE 40



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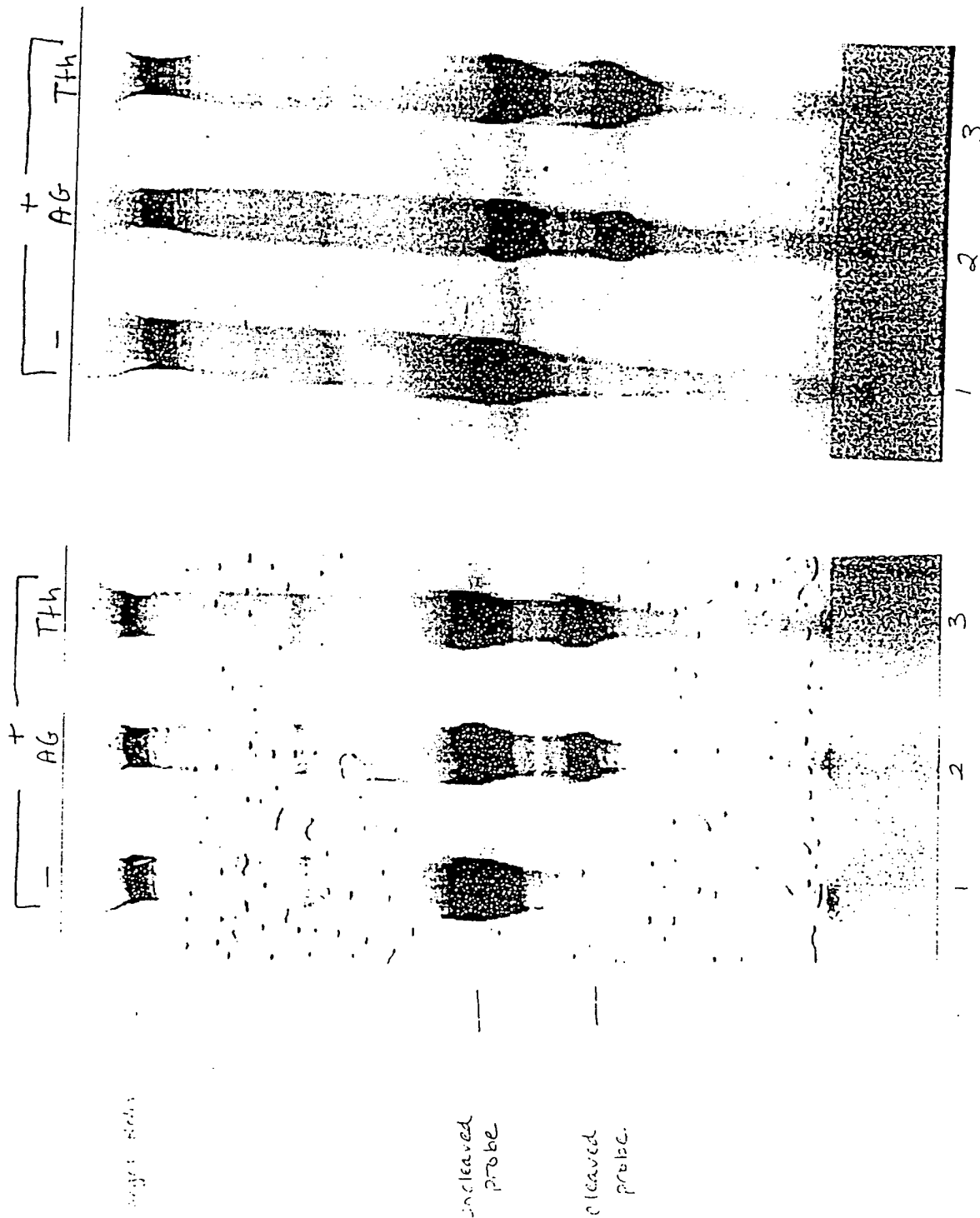
FIGURE 41



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[illegible]

**FIGURE 42B**



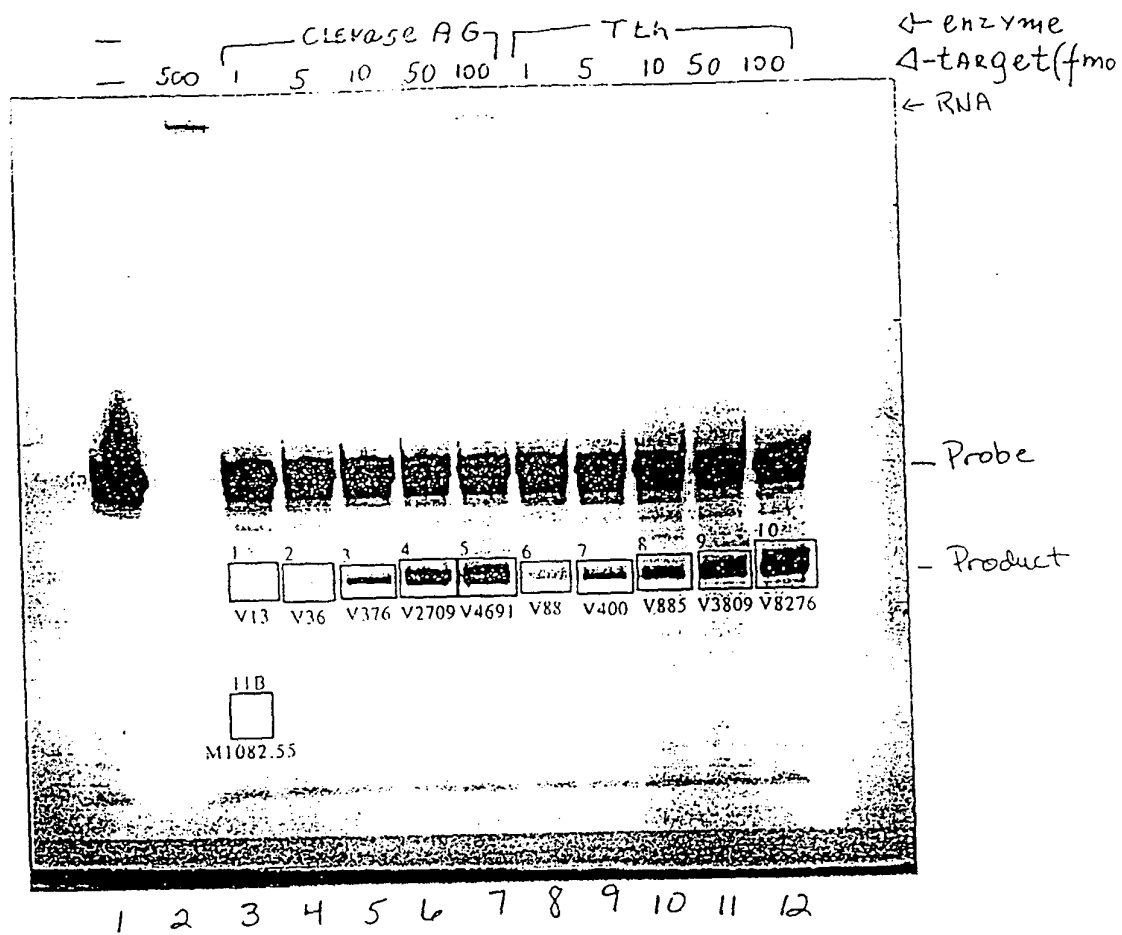


FIGURE 43

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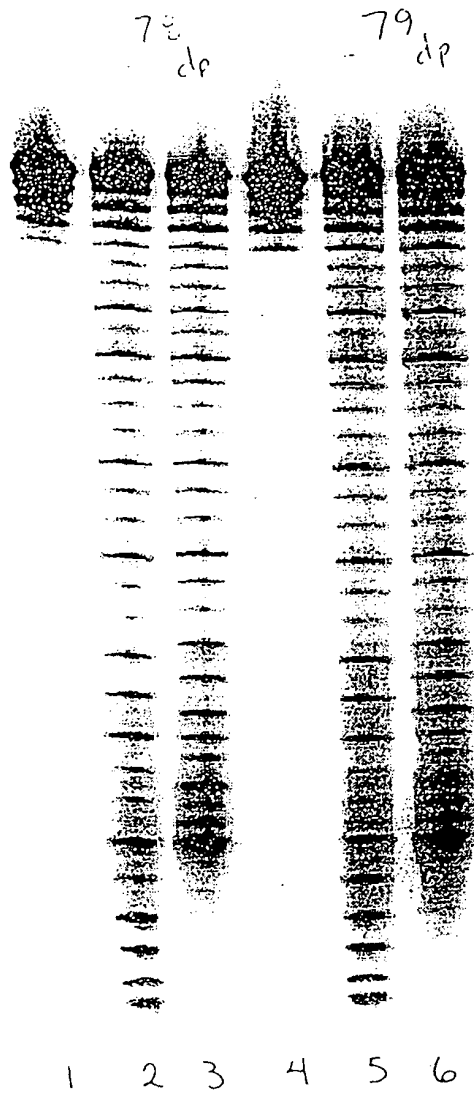


FIGURE 44

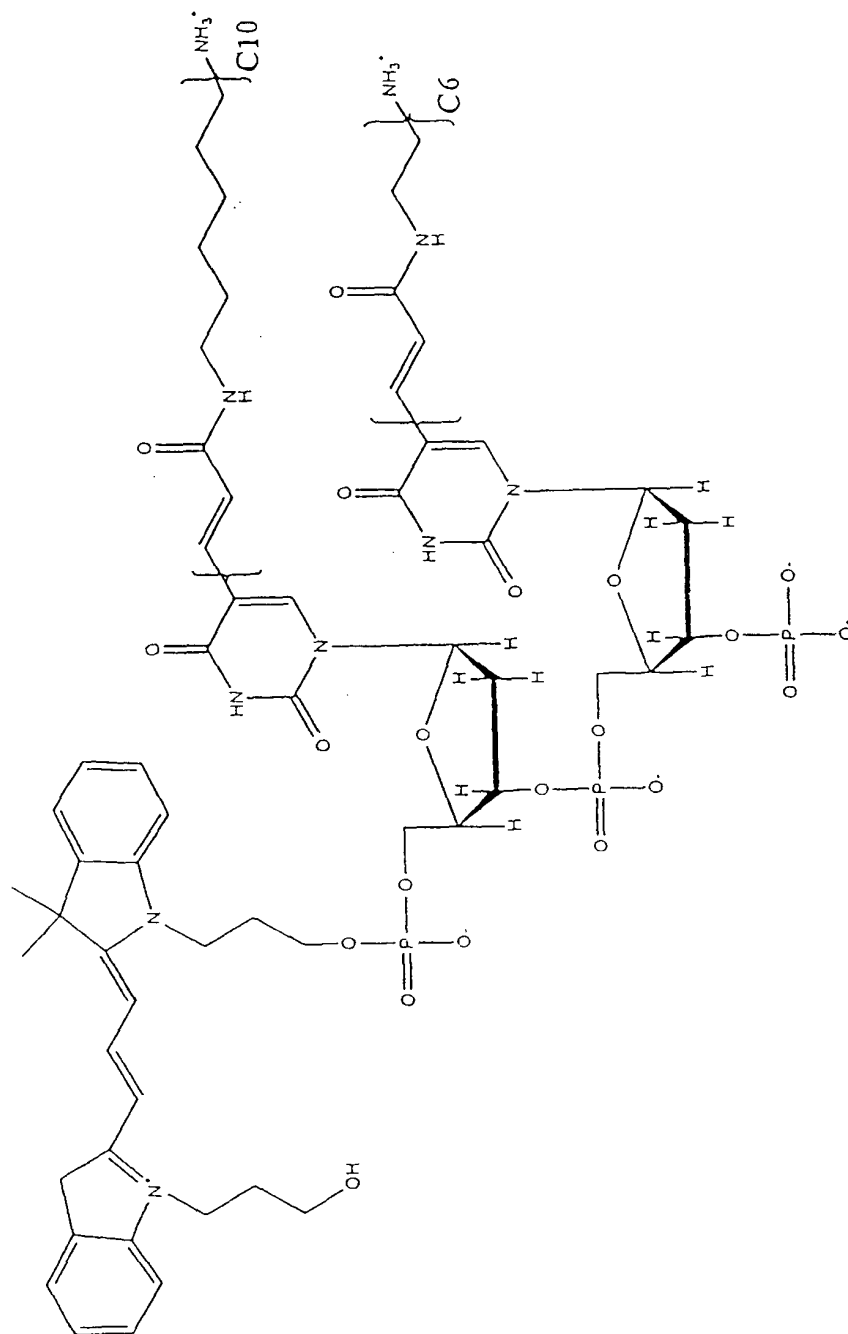
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FIGURE 45

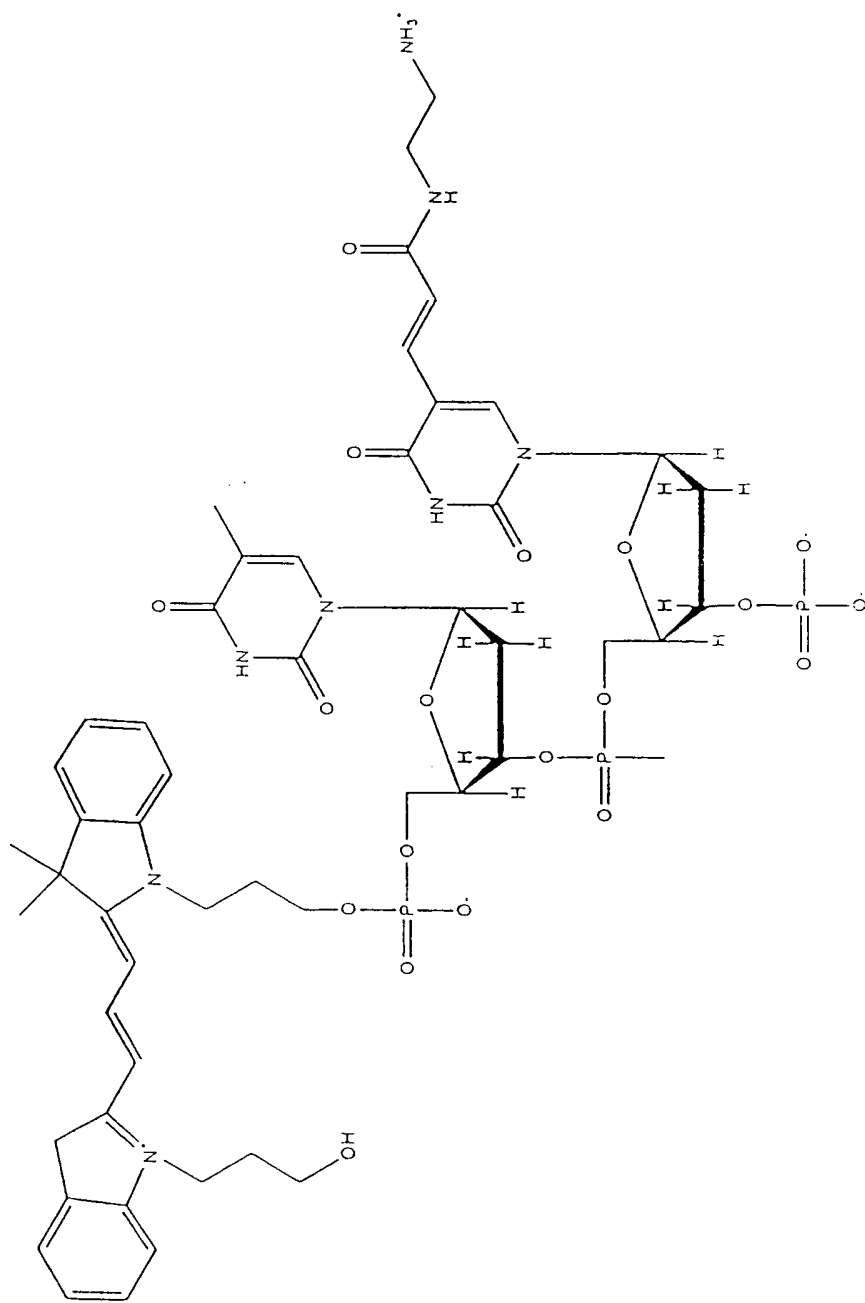
70 (C10 aminoT's)  
74 (C6 amino T's)



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FIGURE 46

75



[illegible]

76

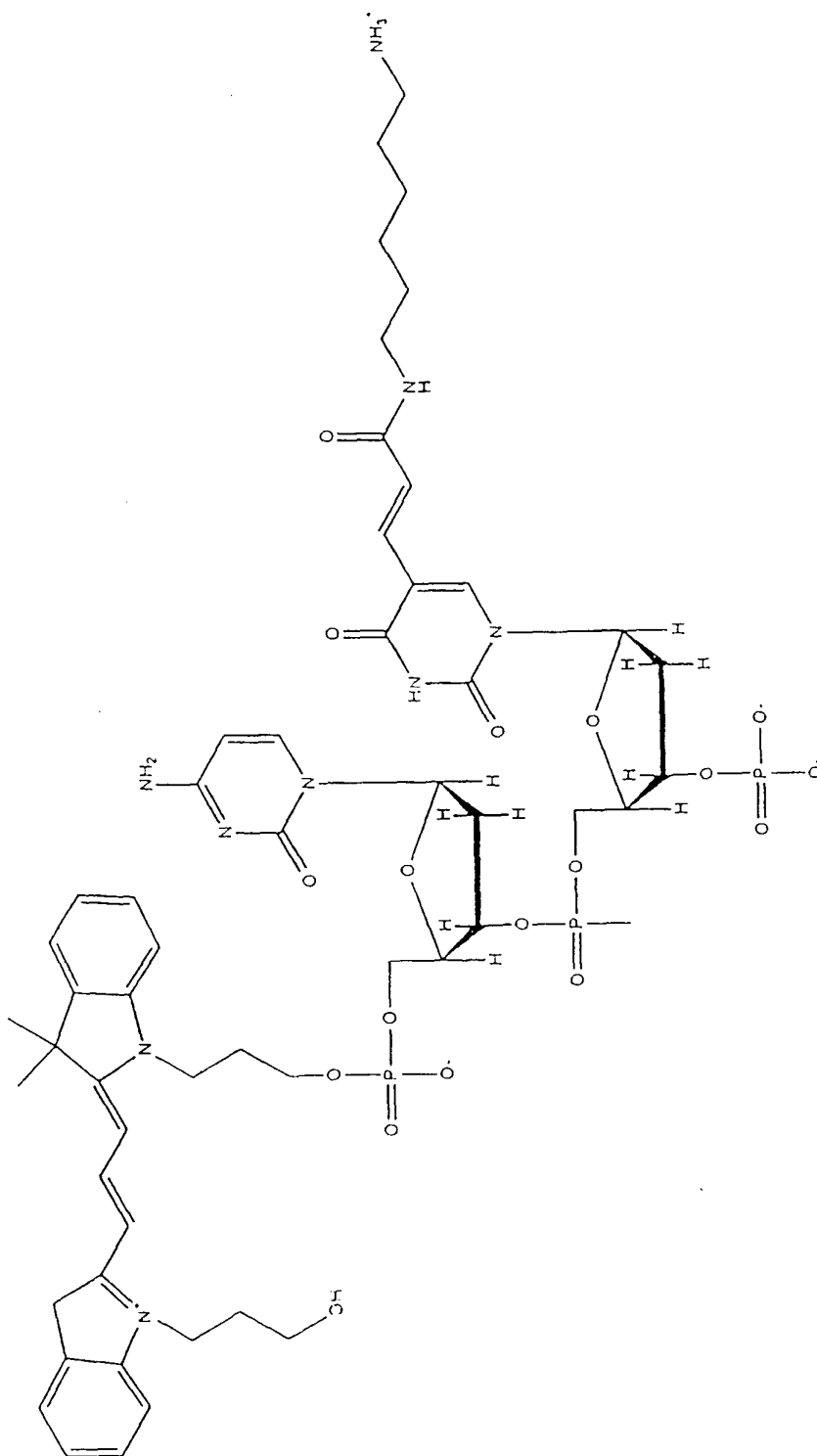
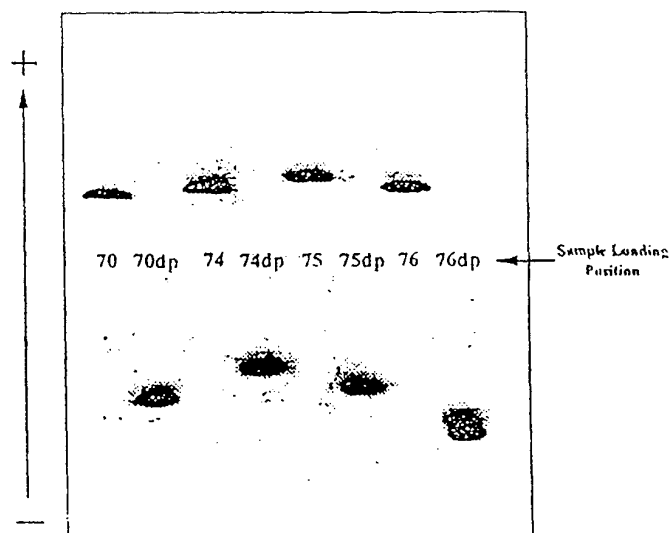


FIGURE 48



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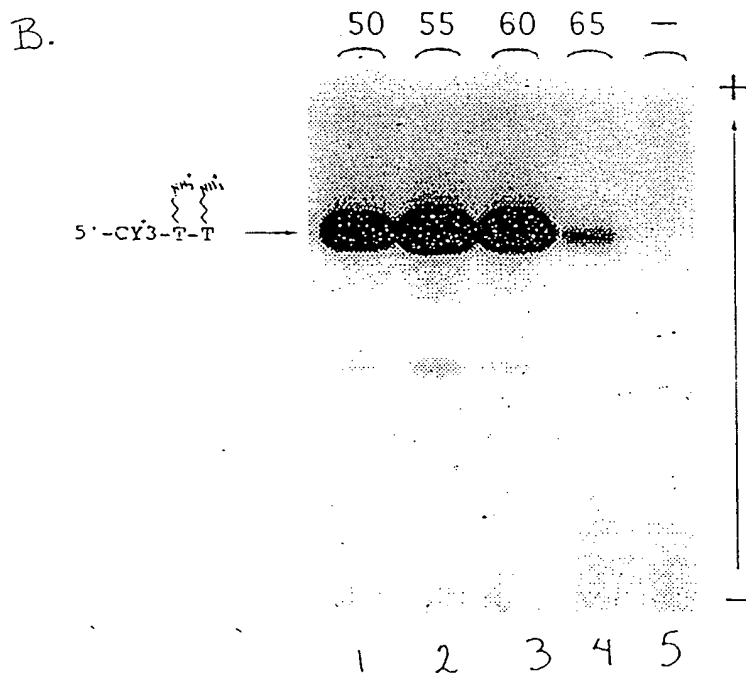
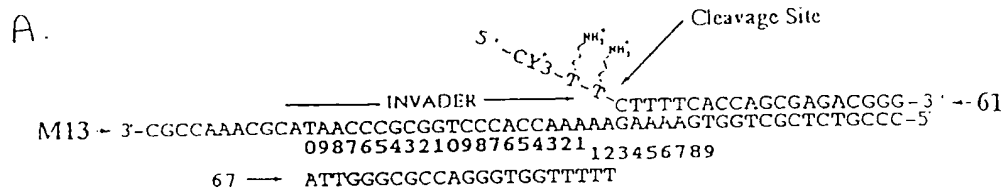
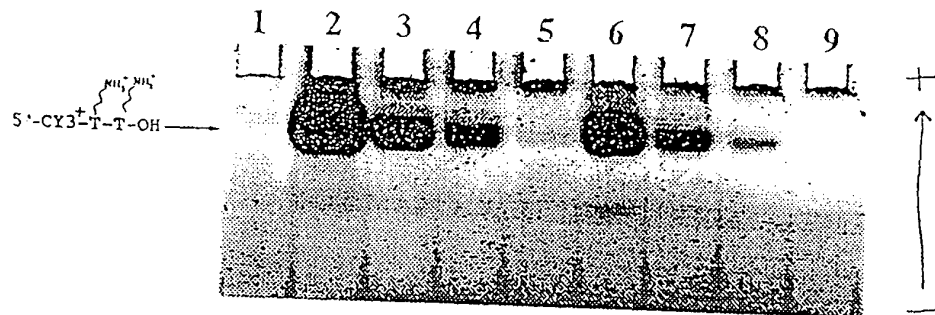


FIGURE 49

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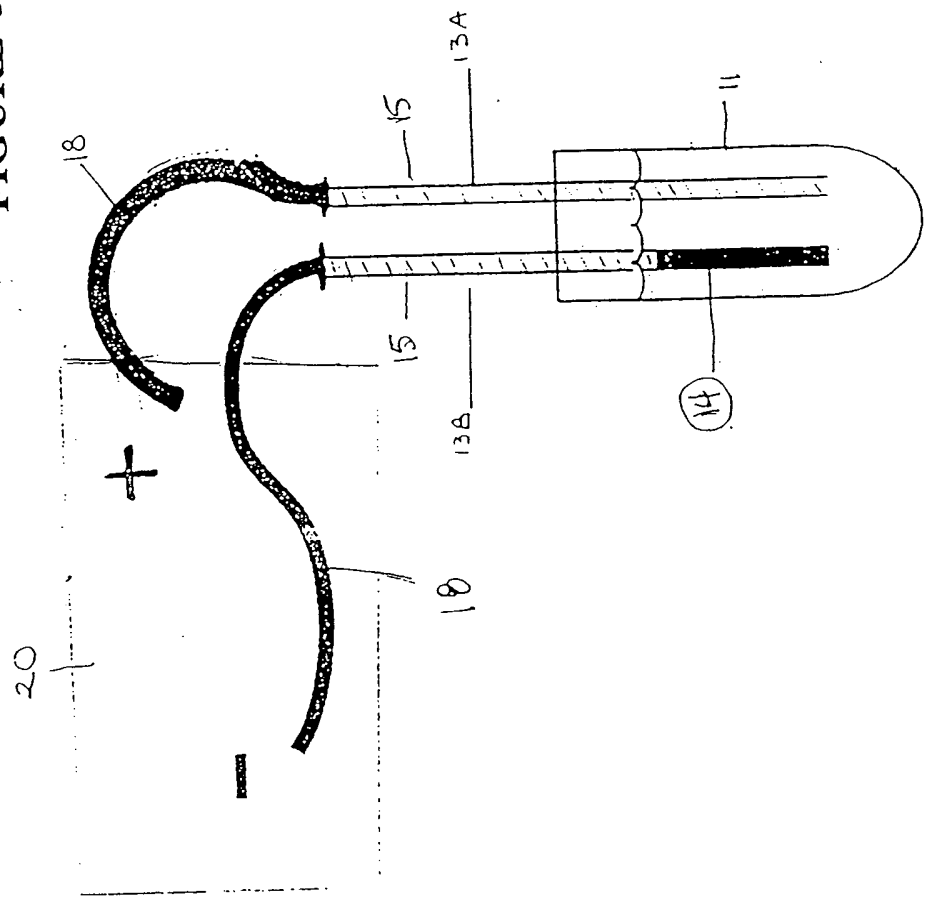
FIGURE 50



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FIGURE 51



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FIGURE 52

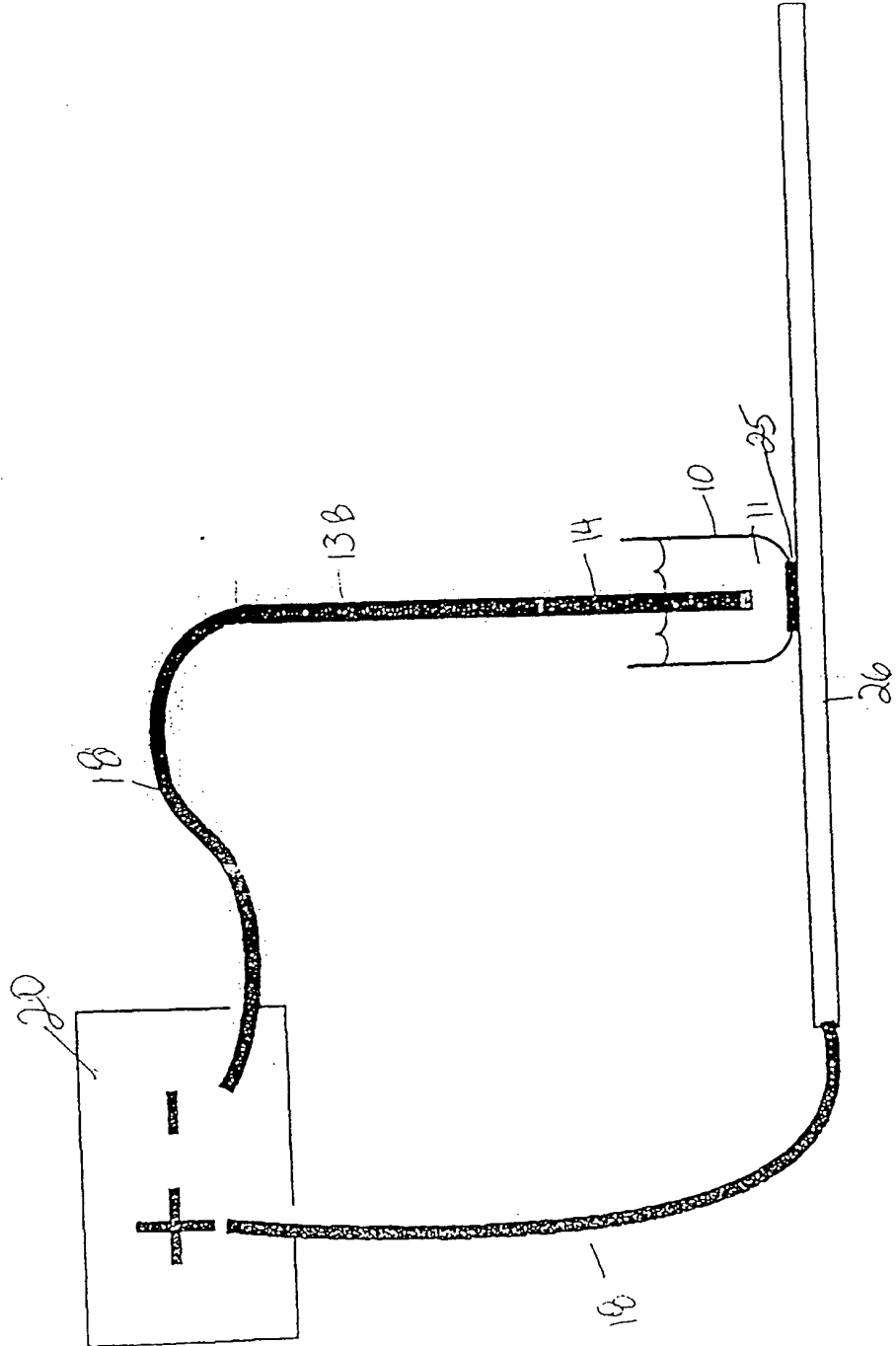
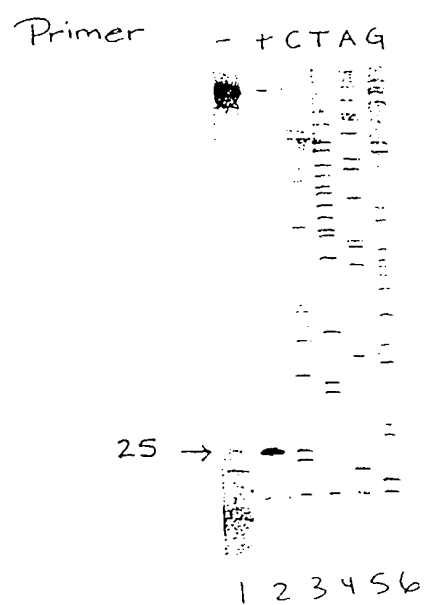




FIGURE 53



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5' AGAAAGGAAGGGAAGAAAGCGAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

AGAAAGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

a

5' CAG AAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGAAGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

b

5' CAGGG GGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGGGGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

c

5' CAGGGTAC AGGGAAGAAAGCGAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

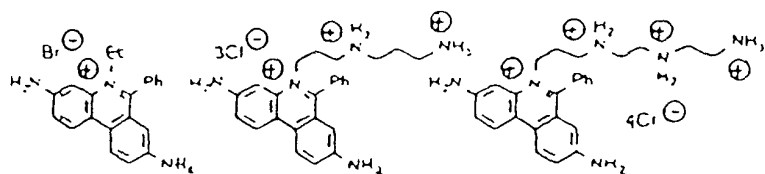
CAGGGTAC  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

d

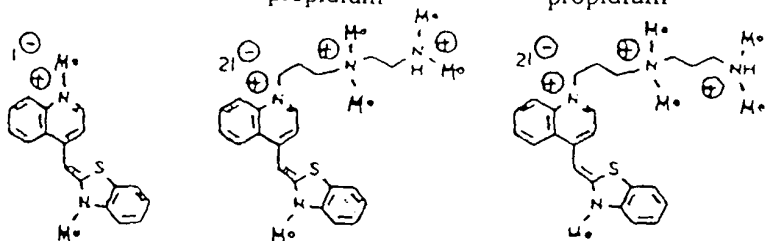
FIGURE 54

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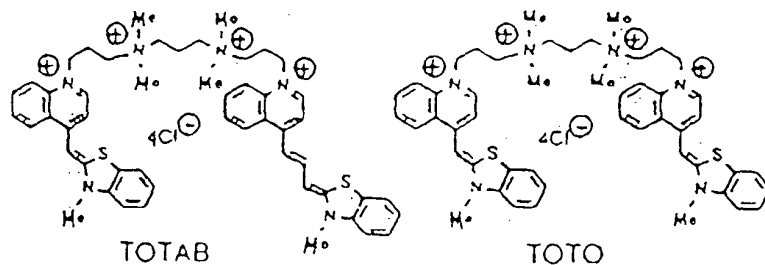
FIGURE 55



Ethidium Bromide (1,3-propanediamino)-propidium (diethylenetriamino)-propidium

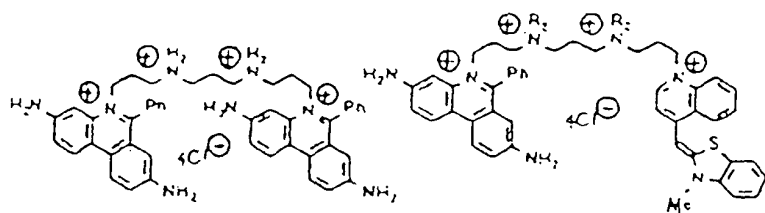


Thiazole Orange (N,N'-tetramethyl-1,2-ethanediamino)-propyl thiazole orange (N,N'-tetramethyl-1,3-propanediamino)-propyl thiazole orange



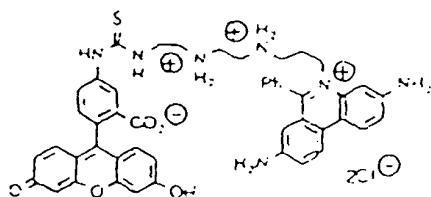
TOTAB

TOTO



EtHd

TOED1 (R = H)  
TOED2 (R = CH<sub>3</sub>)

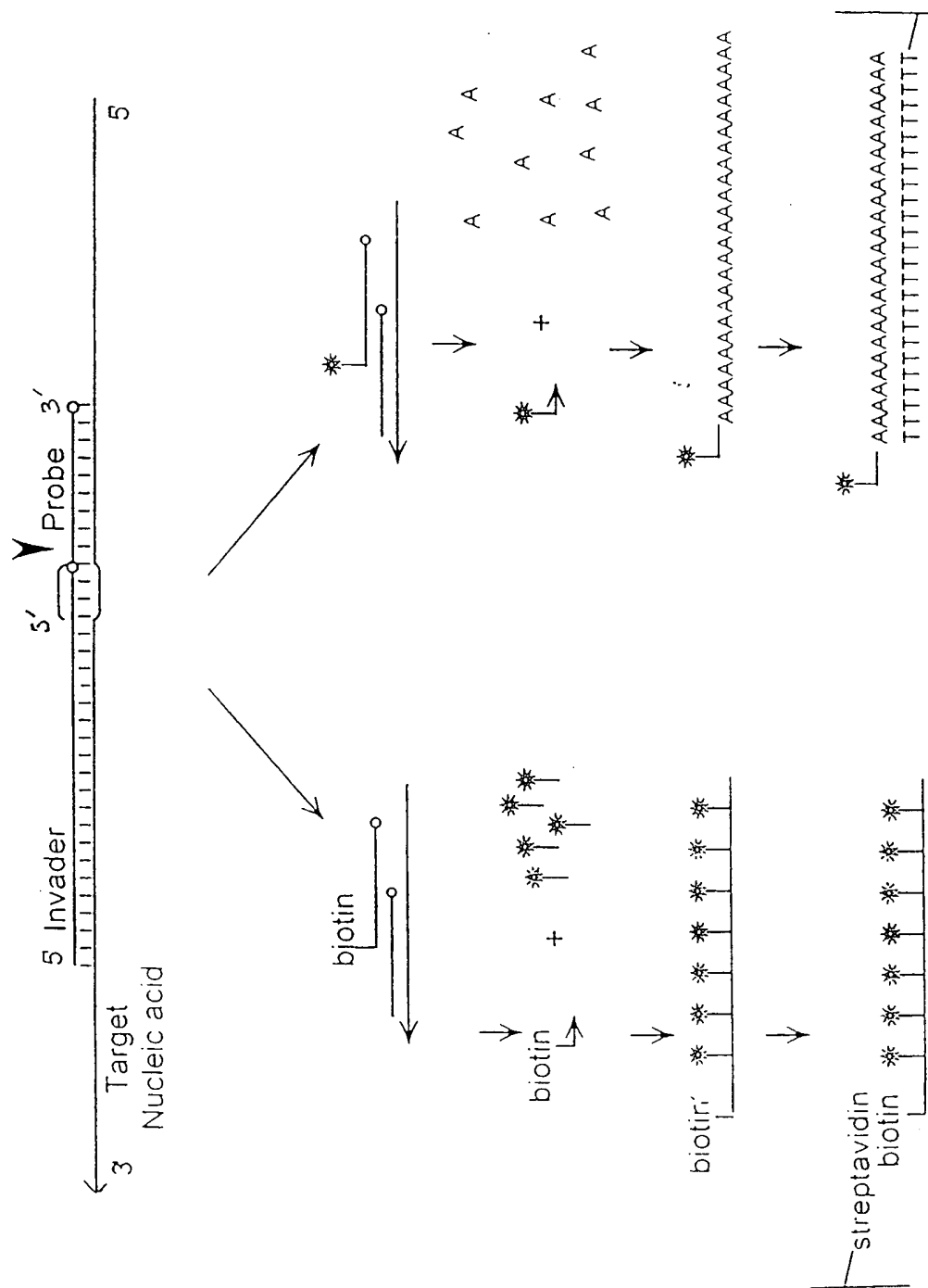


FED

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FIGURE 56



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FIGURE 57

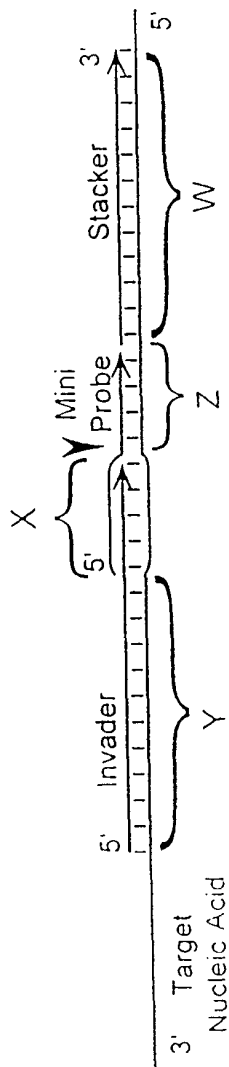
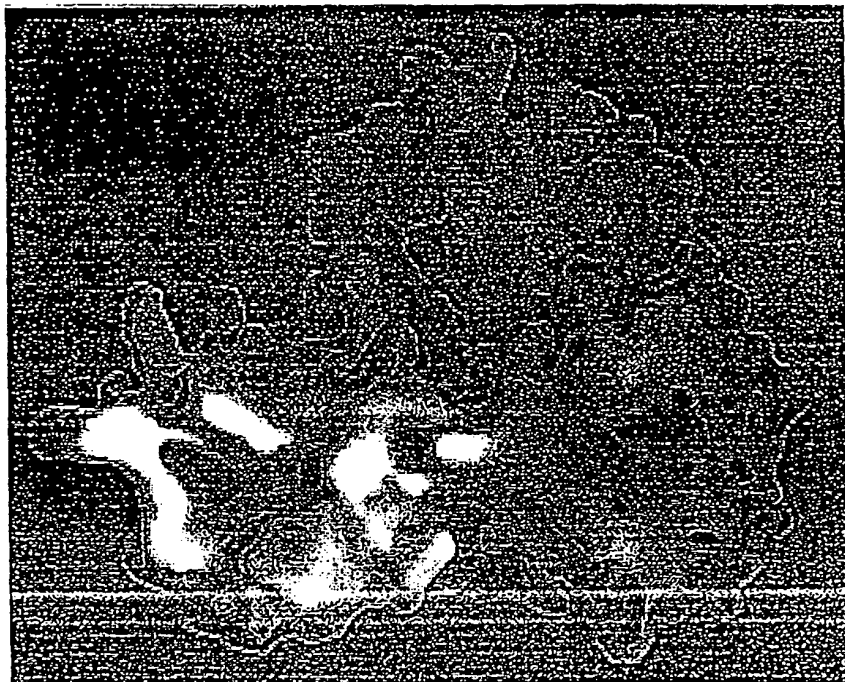


FIGURE 58



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[illegible][illegible][illegible]

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SECRET

FIGURE 59B

150	160	170	180	190	200	210
YVHCKYLLSLMGIPYVEAPSEGEAOAS	YMAKKGDVAVVSODYDALLYGAPRVVRNL	TTTKEM----				MJAFEN1 PRO
LEDAKLLLELMGIPVQAPSEGEAOAA	YMAKGSVYASASODYDSLLFGAPRLVRNL	ITGKRKLPGK				PFUFEN1 PRO
YHDECKHLLSLMGIPYLDAPSEAEASCAAL	VKAGKVYAAATEDMDCLTFGSPVLMRHL	TASEAKKLPIO				HUMFEN1 PRO
YHDECKHLLSLMGIPYLDAPSEAEASCAAL	AKAGKVYAAATEDMDCLTFGSPVLMRHL	TASEAKKLPIO				MUSFEN1 PRO
YHDECKHLLSLMGIPYIAPTAEAOCAEL	AKKGKVYAAASEMDTLCYRTPFLLRHL	TFSEAKKEPIH				YST510 PRO
YHDECKHLLSLMGIPYITAPMEAOCAEL	LOLNLVDGIIIDDSOVFLFGGKIYKNMFHEKNY	-----VE				YSTRAD2 PRO
YHDECKHLLSLMGIPYIVAPOEAOCSKLL	LEKLVDGIVTDDSDVFLFGGTRVYRNMFNQKF	-----VE				SPORAD13 PRO
YHDECKHLLSLMGIPYIOAPMEAOCAILD	TDOTSGTITDDSDIWLFGARHVYRNFNKNKF	-----VE				HUMXPG PRO
YHDECKHLLSLMGIPYIOAPMEAOCAVL	DSOTSGTITDDSDIWLFGARHVYKFNKNKF	-----VE				MUSXPG PRO
YHDECKHLLSLMGIPYIVAPMEAOCAILD	TDOTSGTITDDSDIWLFGARHVYKFNKNKF	-----VE				XENXPG PRO
YHDECKHLLSLMGIPYIVAPMEAOCAILD	TDOTSGTITDDSDIWLFGARHVYKFNKNKF	-----VE				CELRAD2 PRO

220	230	240	250	260	270	280
YVHCKYLLSLMGIPYVEAPSEGEAOAS	YMAKKGDVAVVSODYDALLYGAPRVVRNL	TTTKEM----				MJAFEN1 PRO
LEDAKLLLELMGIPVQAPSEGEAOAA	YMAKGSVYASASODYDSLLFGAPRLVRNL	ITGKRKLPGK				PFUFEN1 PRO
YHDECKHLLSLMGIPYLDAPSEAEASCAAL	VKAGKVYAAATEDMDCLTFGSPVLMRHL	TASEAKKLPIO				HUMFEN1 PRO
YHDECKHLLSLMGIPYLDAPSEAEASCAAL	AKAGKVYAAATEDMDCLTFGSPVLMRHL	TASEAKKLPIO				MUSFEN1 PRO
YHDECKHLLSLMGIPYIAPTAEAOCAEL	AKKGKVYAAASEMDTLCYRTPFLLRHL	TFSEAKKEPIH				YST510 PRO
YHDECKHLLSLMGIPYITAPMEAOCAEL	LOLNLVDGIIIDDSOVFLFGGKIYKNMFHEKNY	-----VE				YSTRAD2 PRO
YHDECKHLLSLMGIPYIVAPOEAOCSKLL	LEKLVDGIVTDDSDVFLFGGTRVYRNMFNQKF	-----VE				SPORAD13 PRO
YHDECKHLLSLMGIPYIOAPMEAOCAILD	TDOTSGTITDDSDIWLFGARHVYRNFNKNKF	-----VE				HUMXPG PRO
YHDECKHLLSLMGIPYIOAPMEAOCAVL	DSOTSGTITDDSDIWLFGARHVYKFNKNKF	-----VE				MUSXPG PRO
YHDECKHLLSLMGIPYIVAPMEAOCAILD	TDOTSGTITDDSDIWLFGARHVYKFNKNKF	-----VE				XENXPG PRO
YHDECKHLLSLMGIPYIVAPMEAOCAILD	TDOTSGTITDDSDIWLFGARHVYKFNKNKF	-----VE				CELRAD2 PRO



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-30	440	450	460	470	480	490
MJAFEN1 PRO						
PFUFEN1 PRO						
HUMFEN1 PRO						
GSL S						
MUSFEN1 PRO						
YST510 PRO						
YSTRAD2 PRO						
SPORAD13 PRO						
HUMXPG PRO						
MUSXPG PRO						
XENXPG PRO						
CELRAD2 PRO						

500	510	520	530	540	550	560
MJAFEN1 PRO						
PFUFEN1 PRO						
HUMFEN1 PRO						
MUSFEN1 PRO						
YST510 PRO						
YSTRAD2 PRO						
SPORAD13 PRO						
HUMXPG PRO						
MUSXPG PRO						
XENXPG PRO						
CELRAD2 PRO						

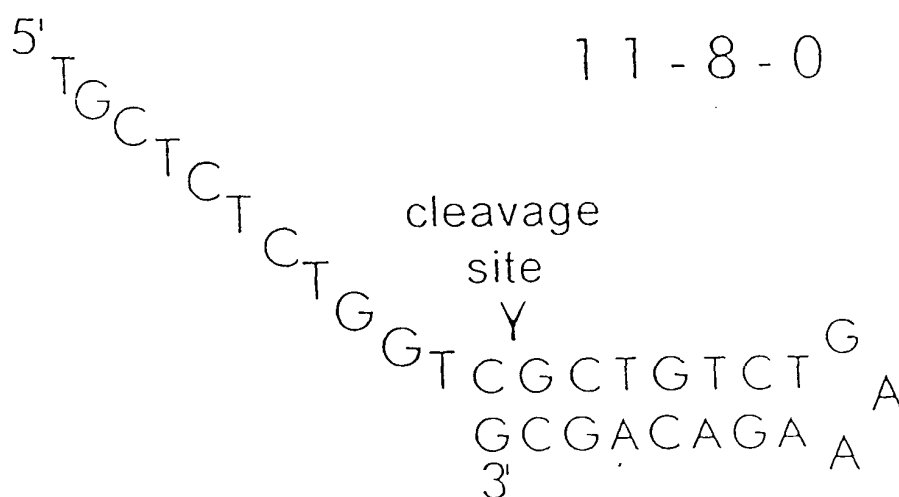
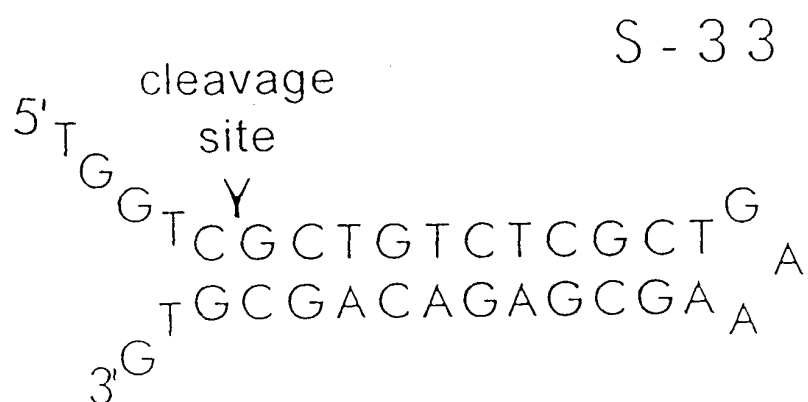
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FIGURE 59E

MJAFEN1 PRO  
PFUFEN1 PRO  
HUMFEN1 PRO  
MUSFEN1 PRO  
YST510 PRO  
YSTRAD2 PRO  
SPORAD13 PRO  
HUMXPG PRO  
MUSXPG PRO  
XENXPG PRO  
CELRAD2 PRO

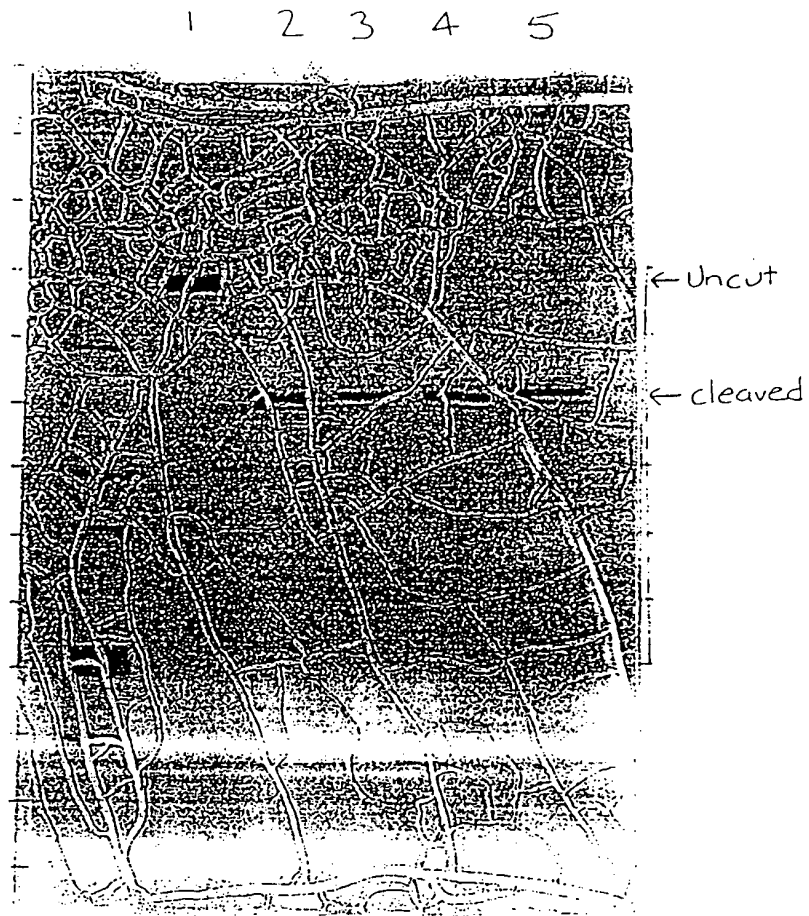
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 60



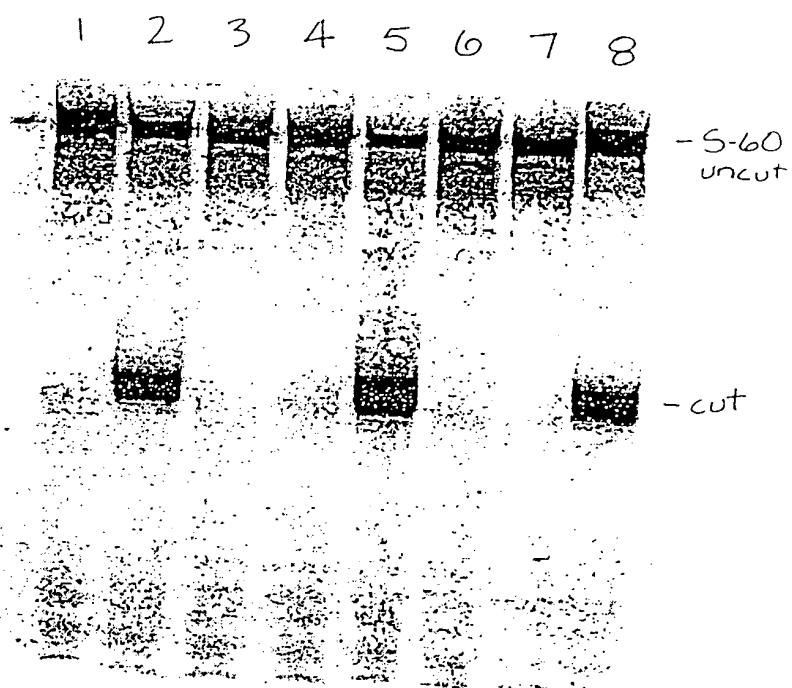
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FIGURE 61



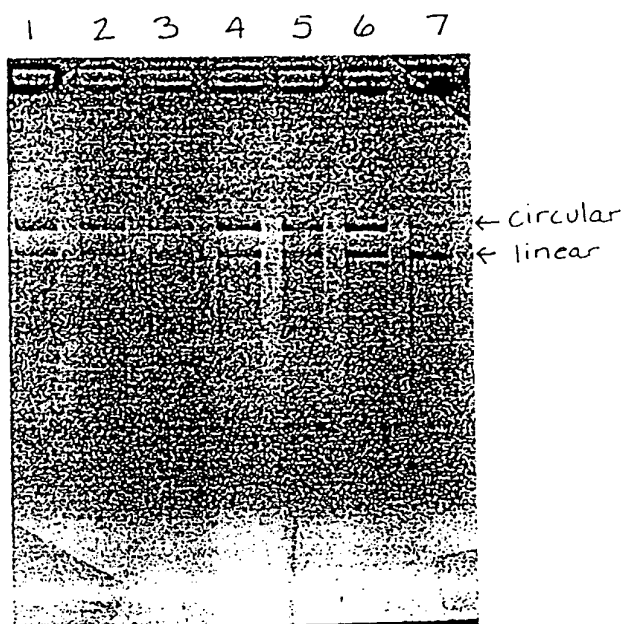
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FIGURE 62



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FIGURE 63



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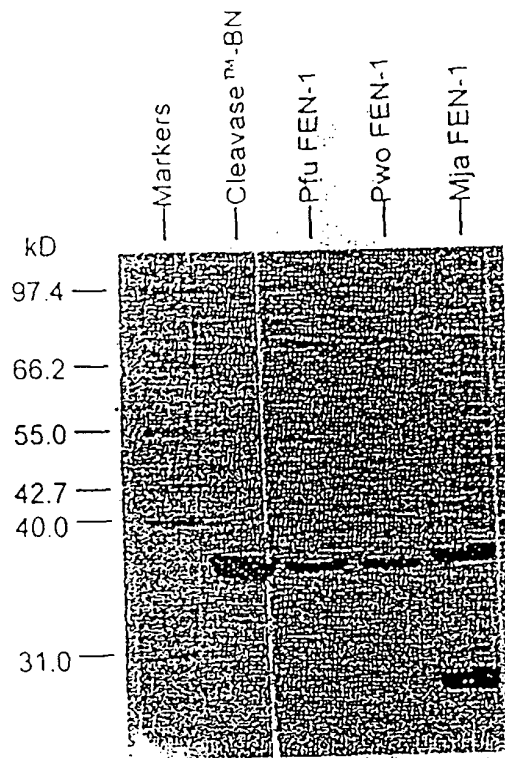
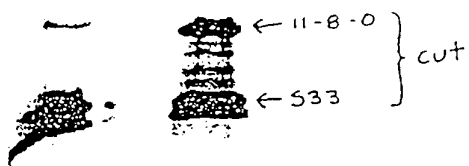
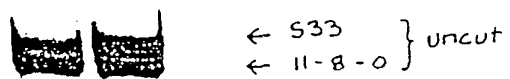


FIGURE 64

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Enzyme      Cleavase<sup>®</sup> — Mja  
                 BN






1    2    3

FIGURE 65

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	+	-	+	-	+	
Terminal Transferase	+	-	+	-	+	
Alkaline Phosphatase	-	-	-	+	+	
Thermal Degradation	-	+	+	+	+	

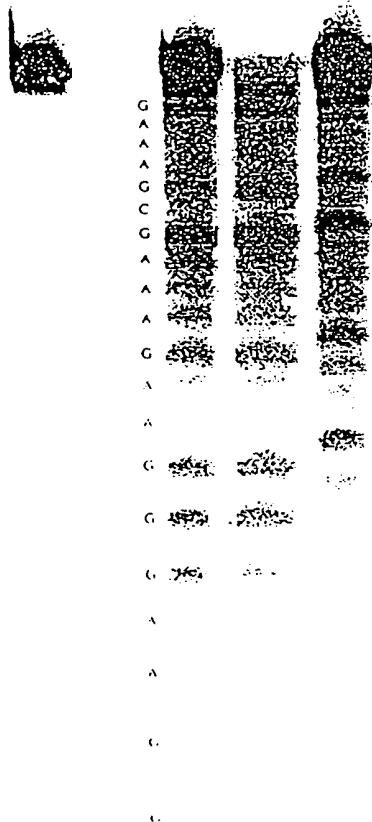


FIGURE 66

5'-nAGAAggaaggggagaaagcgaaagG-3'

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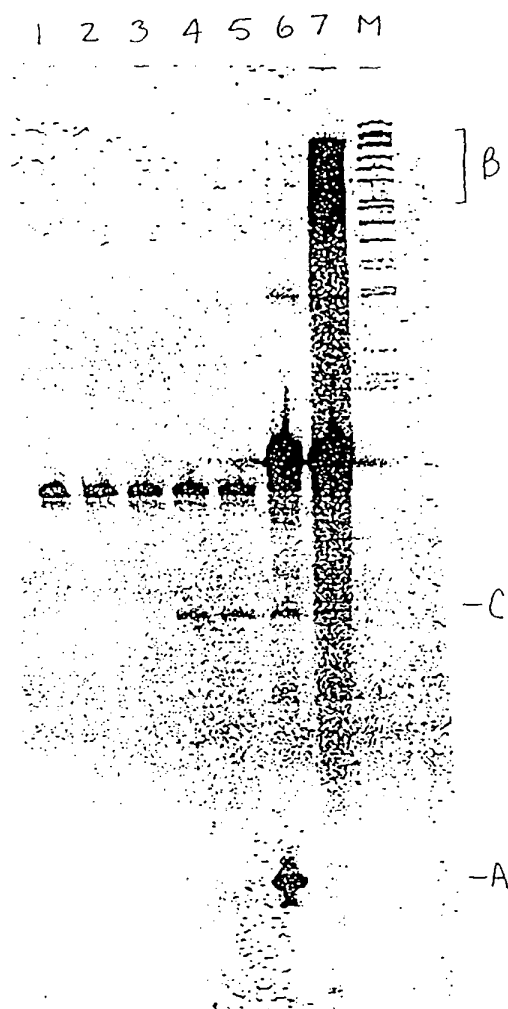


FIGURE 67

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FIGURE 68

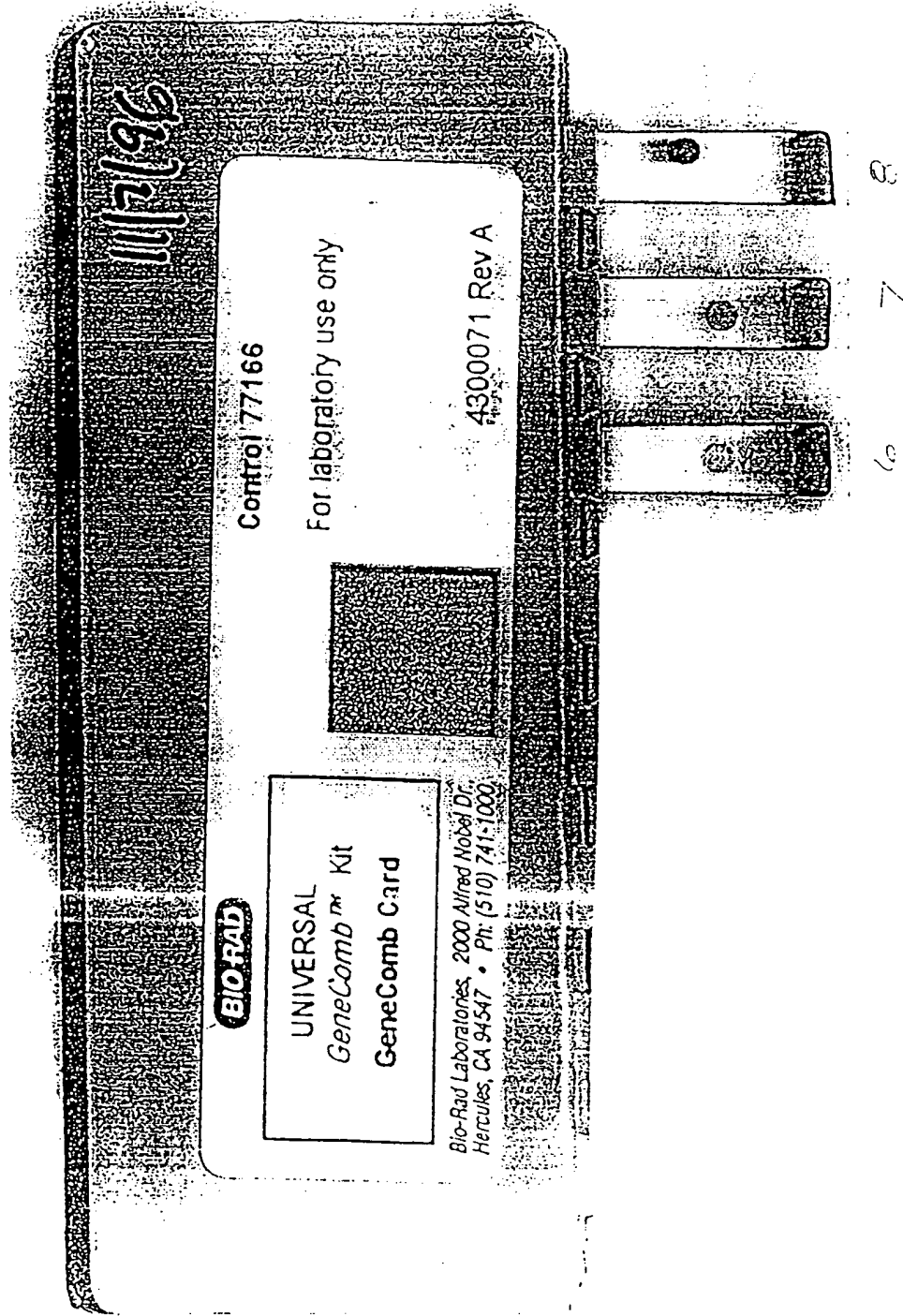


FIGURE 69

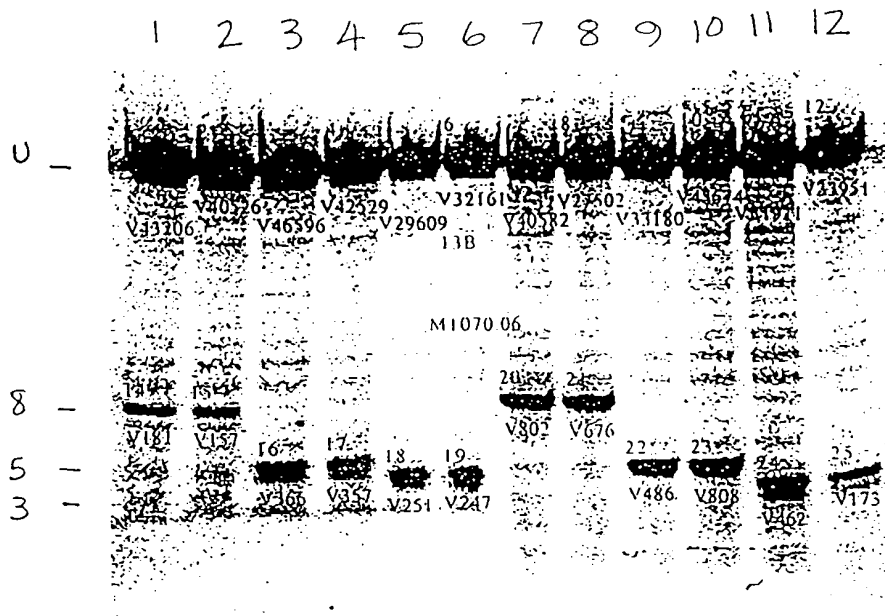


FIGURE 70

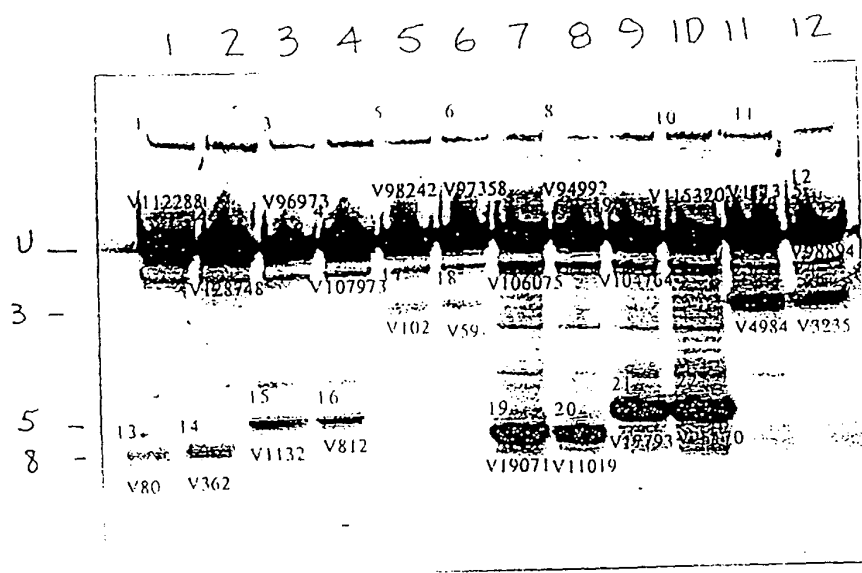
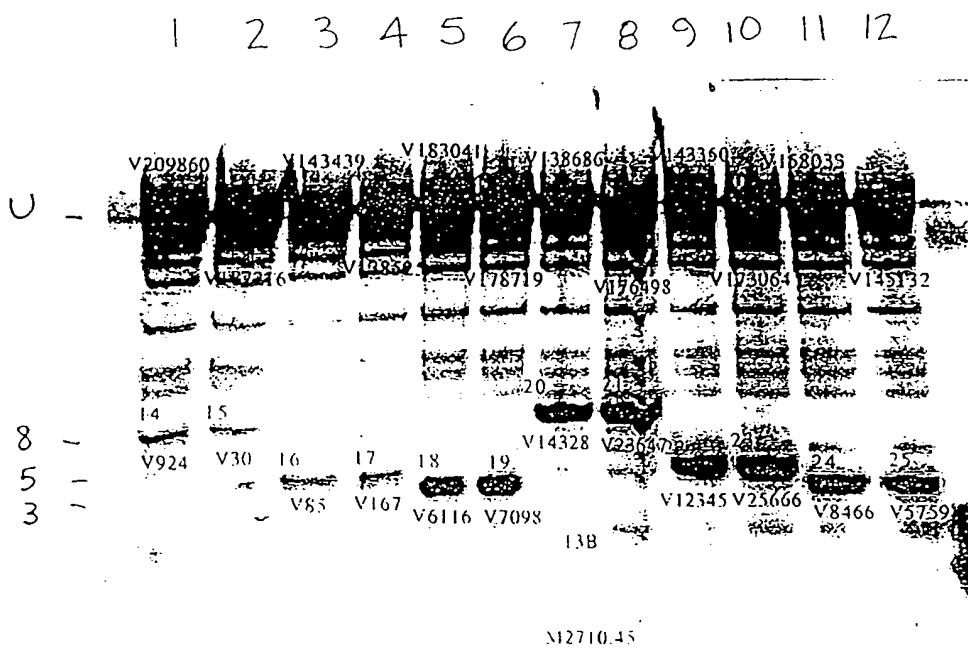
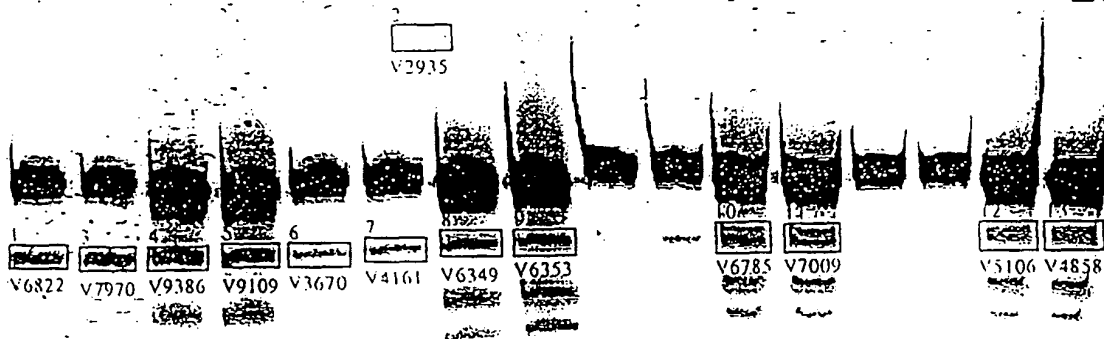


FIGURE 71

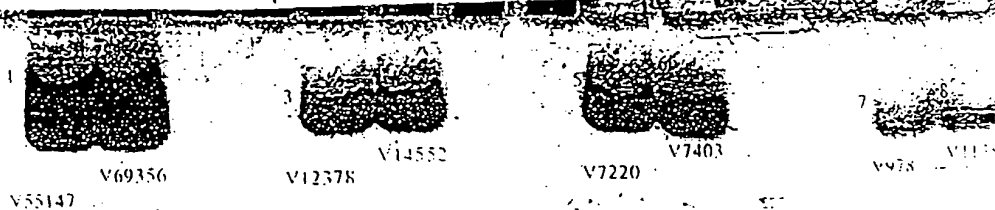


A

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16



B 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16



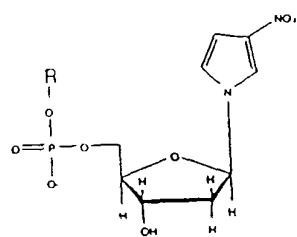
9B

M1347.48

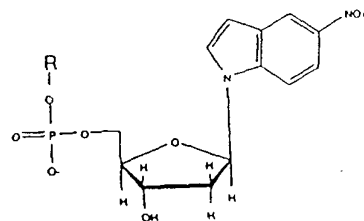
FIGURE 72



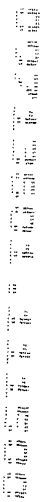
FIGURE 73



3-nitropyrrole



5-nitroindole



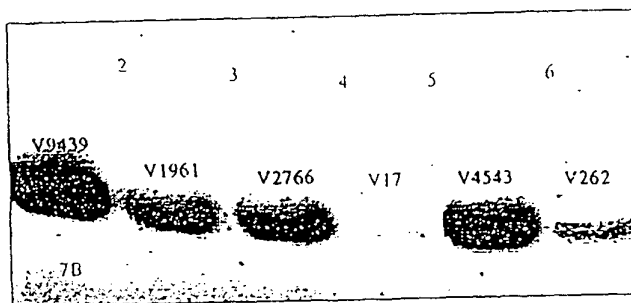
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Allcomp	1Base mismatch	Allcomp	1Base mismatch	Allcomp	1Base mismatch
		2 NI	2 NI	1 NP	1 NP

Inval #	67	114	115	116	112	113
------------	----	-----	-----	-----	-----	-----

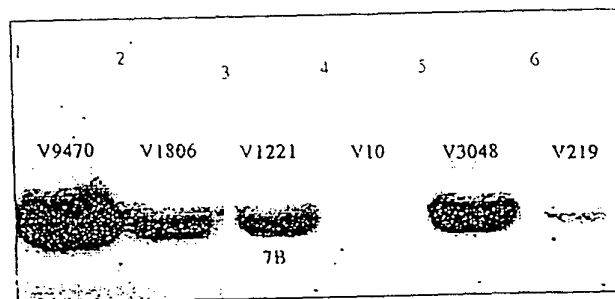
A

52°C



B

55°C



C

58°C

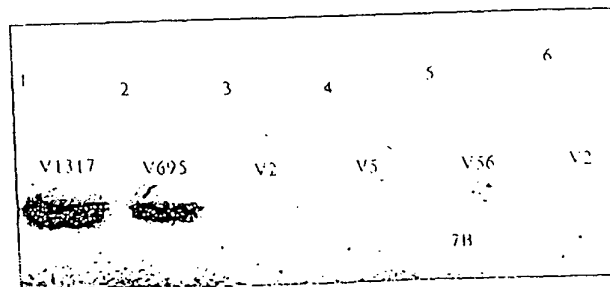


FIGURE 75

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# FIGURE 76

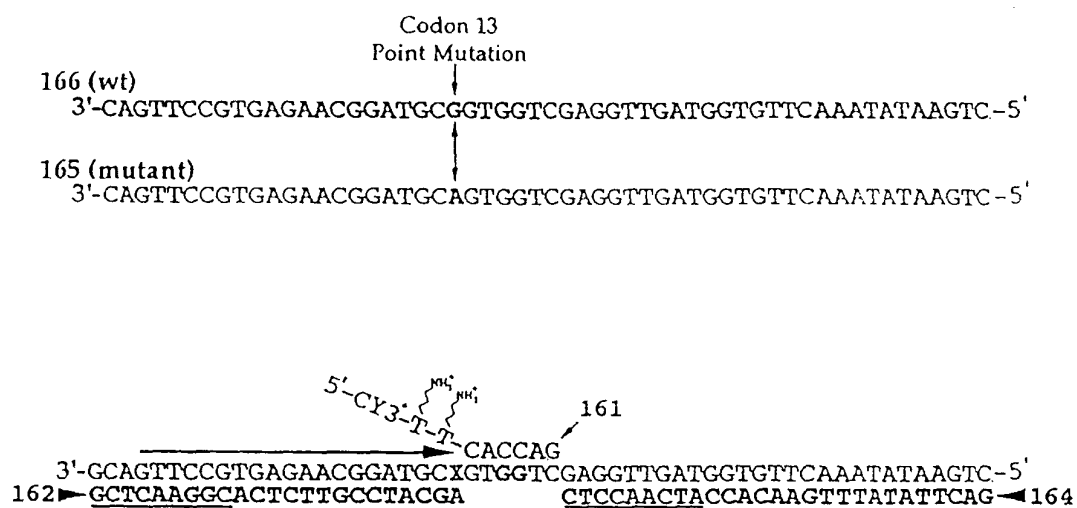
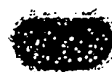


FIGURE 77

Temp	→	47°		50°		53°		56°
Target	→	165	166	165	166	165	166	165 166



**FIGURE 78**



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# Invader 3'-end Substituents

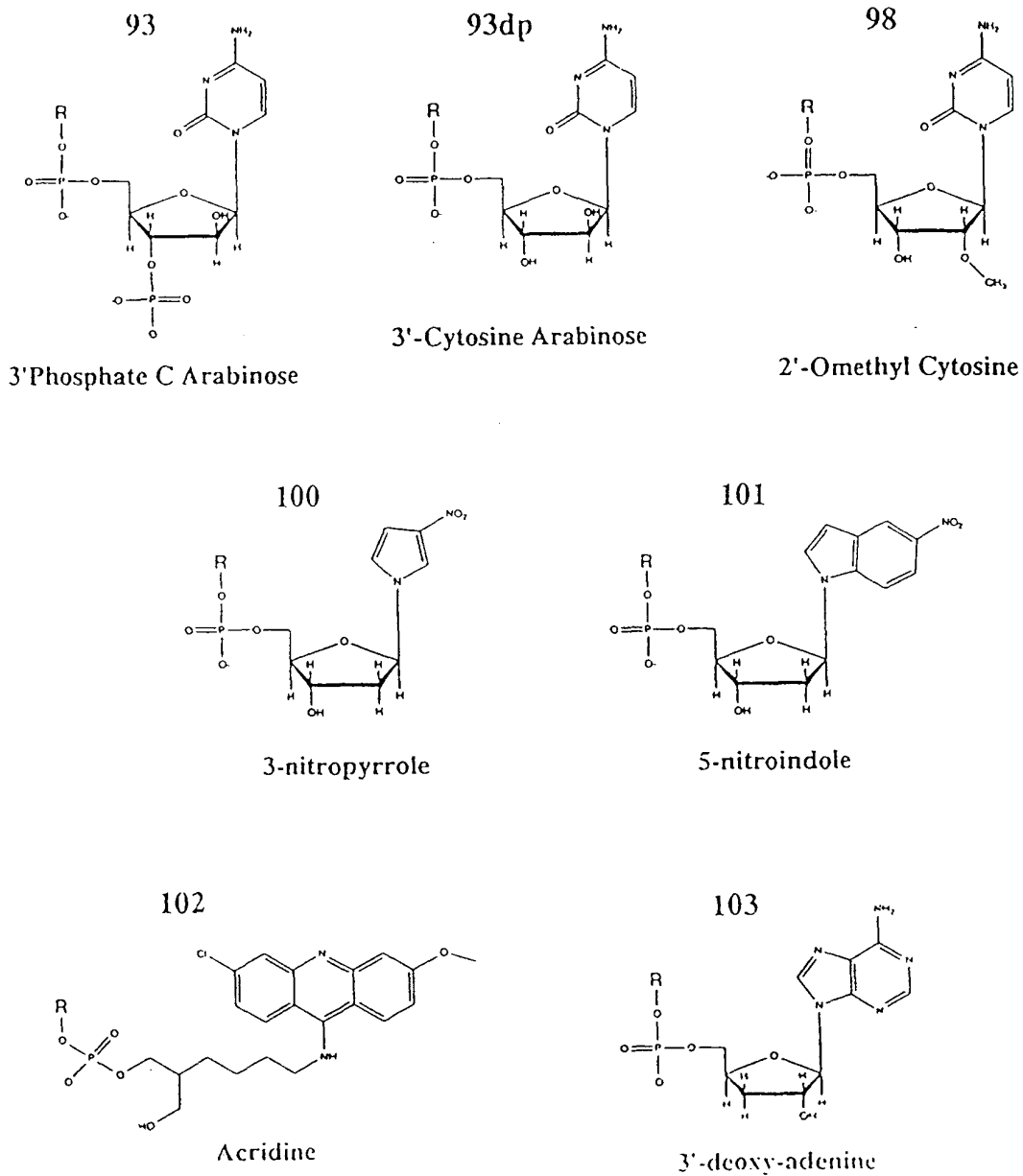


FIGURE 79

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Concentration of Probe w/ and w/o Stacker vs Temp

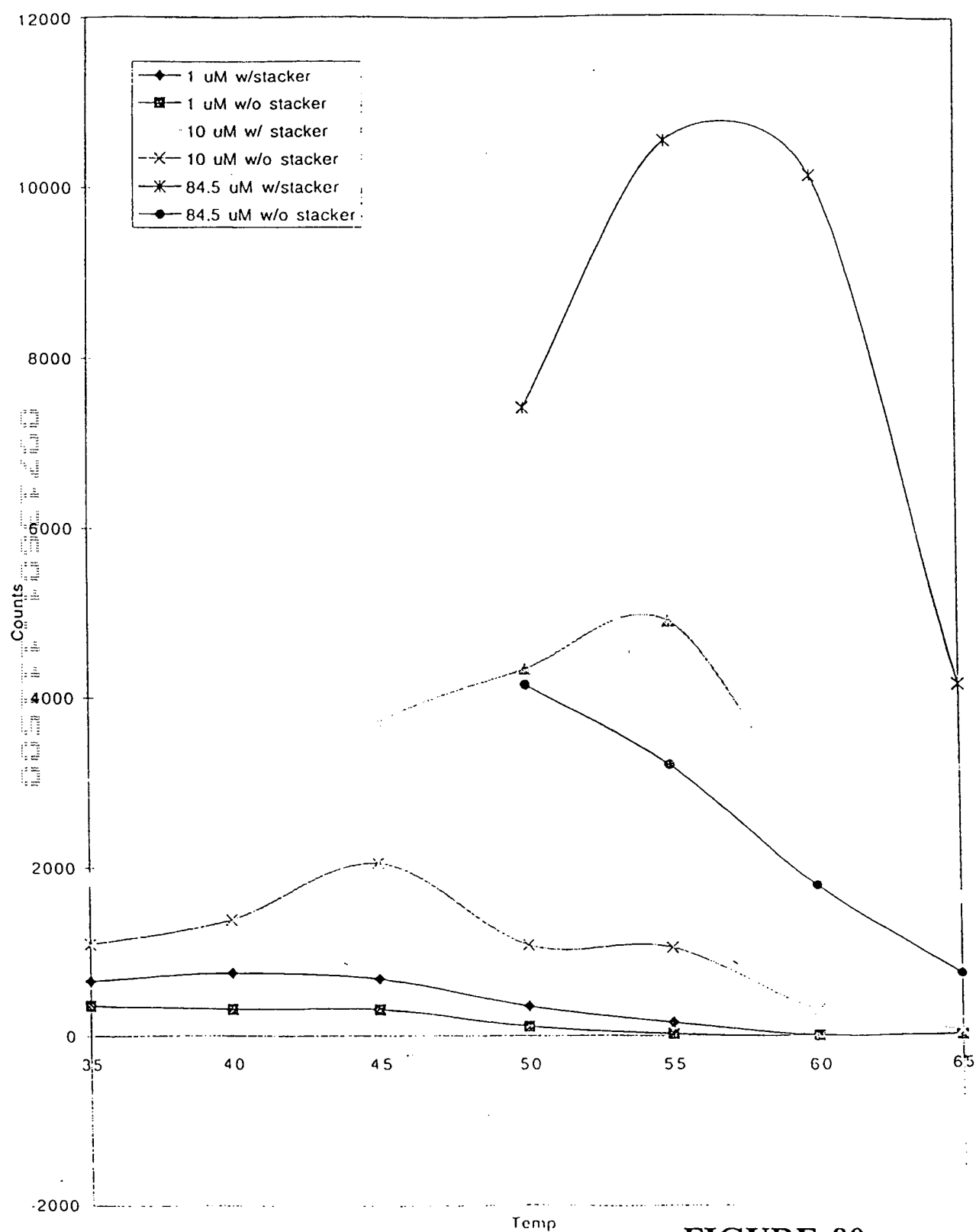


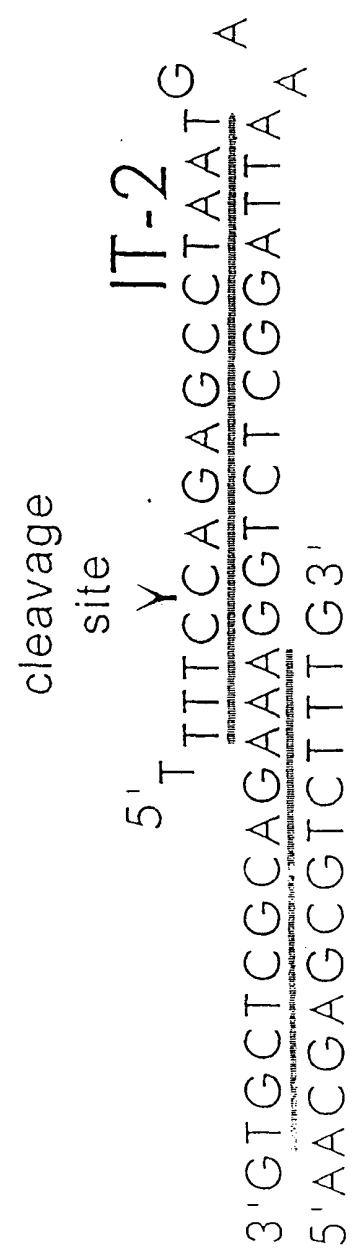
FIGURE 80

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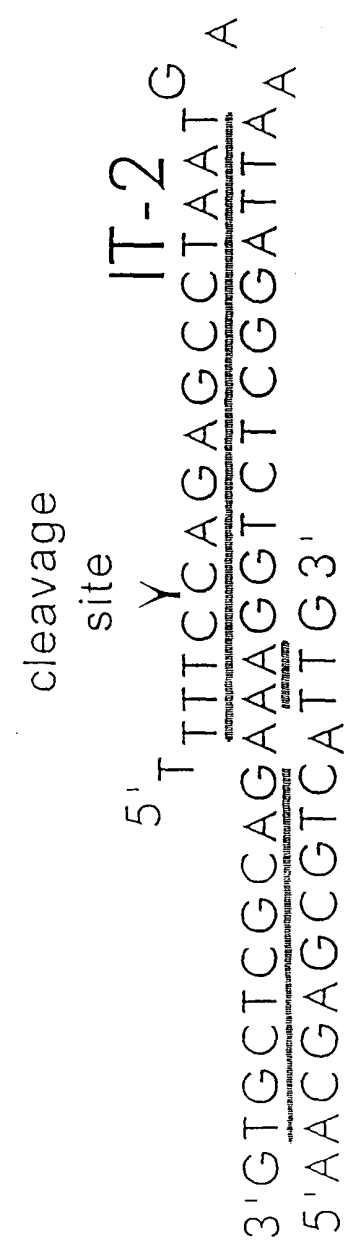


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FIGURE 81



IT-1



IT-1A4

# FIGURE 82

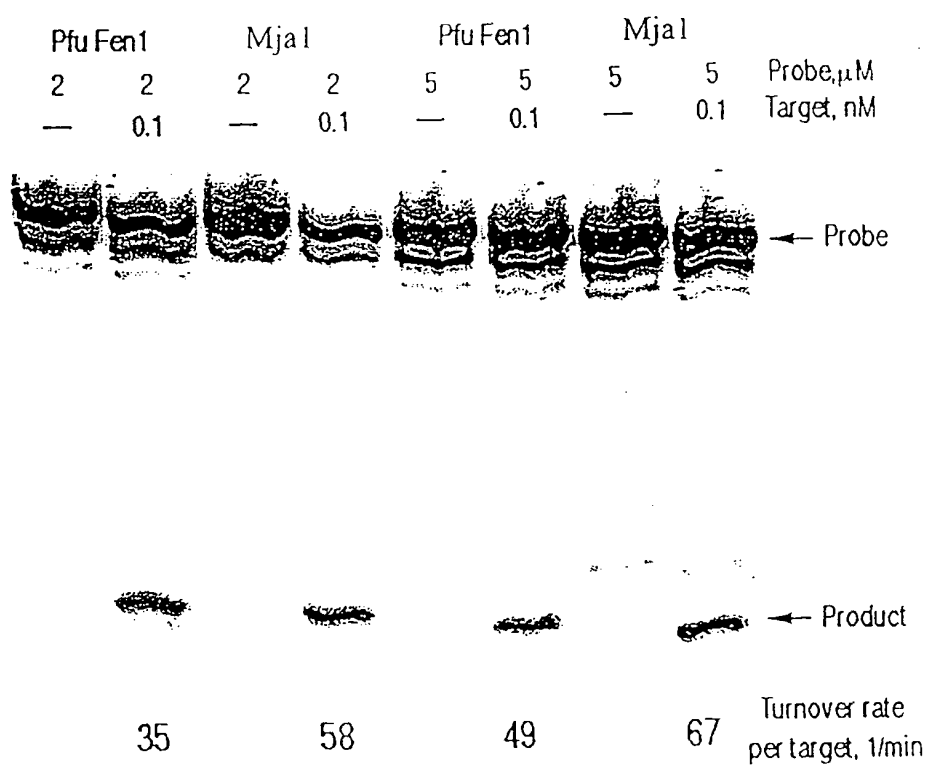
1 2 3 4



—

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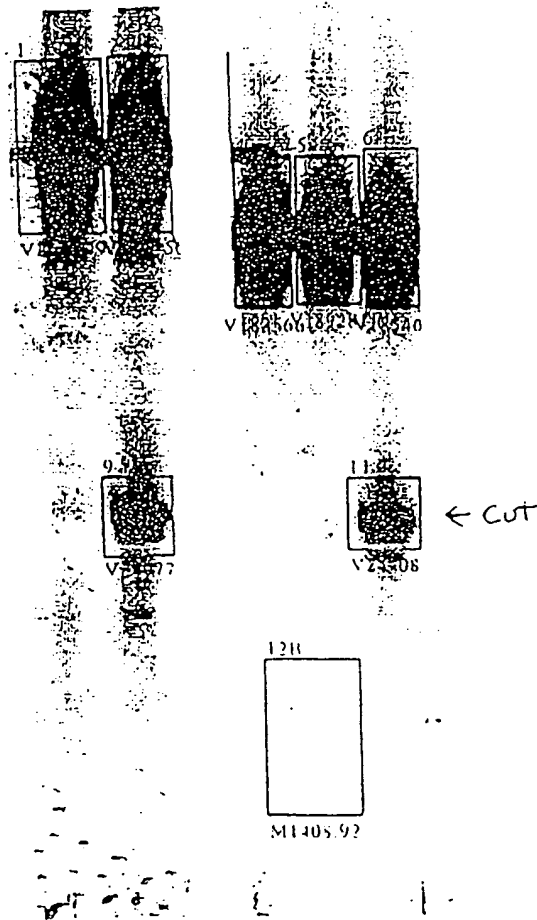
FIGURE 83



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FIGURE 84

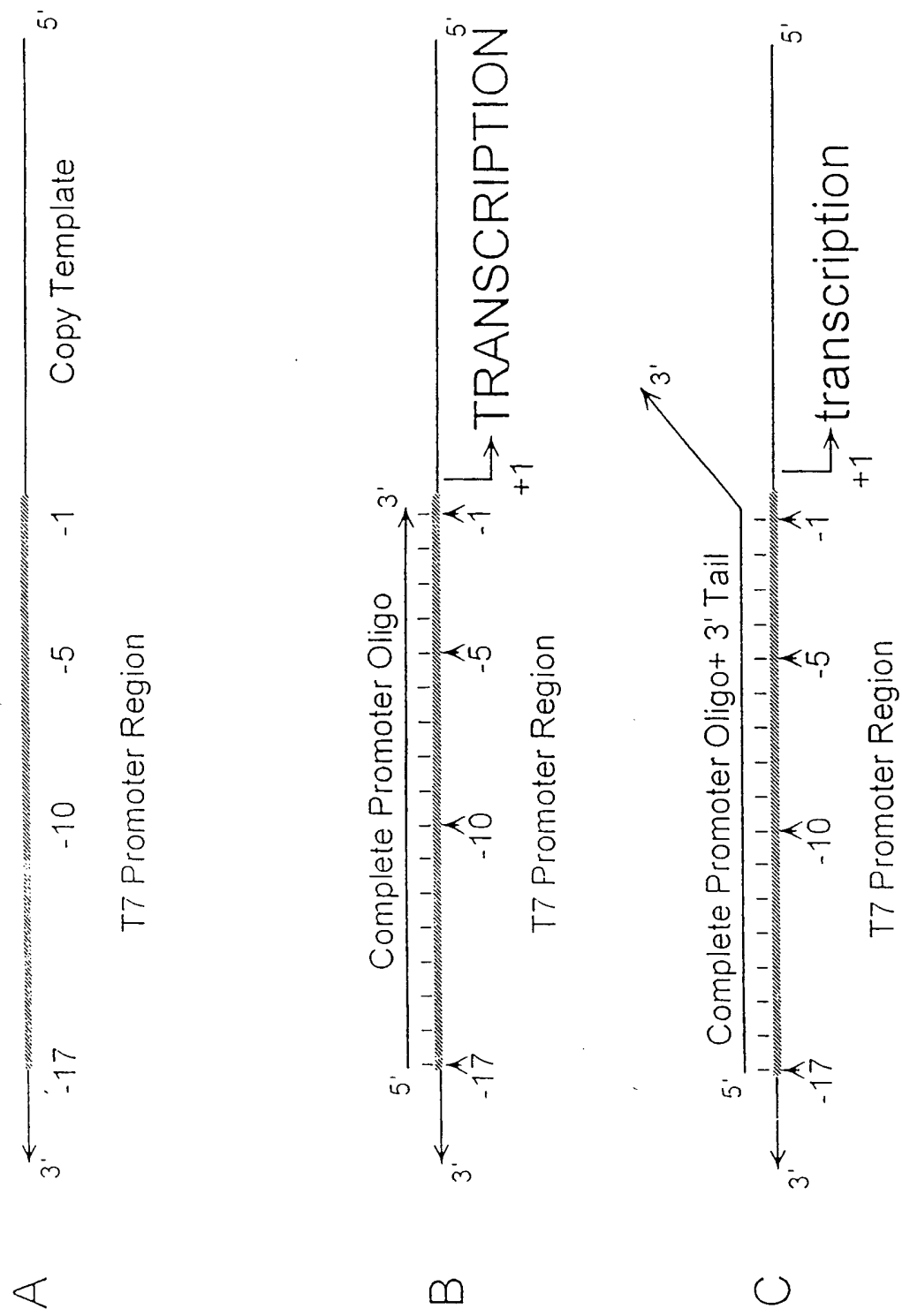
1 2 3 4 5



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FIGURE 85



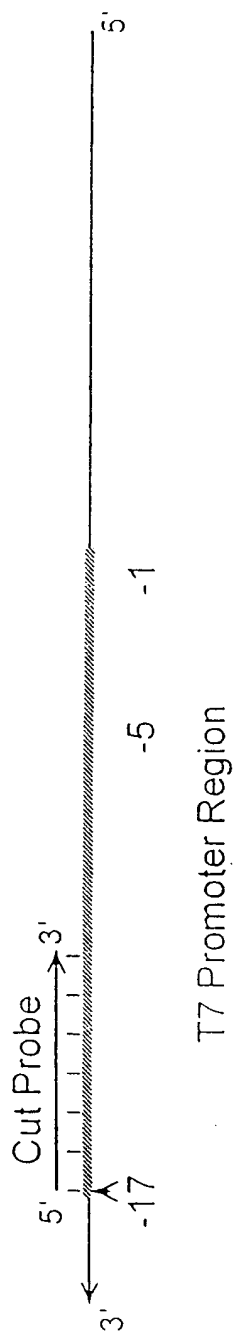


FIGURE 86A

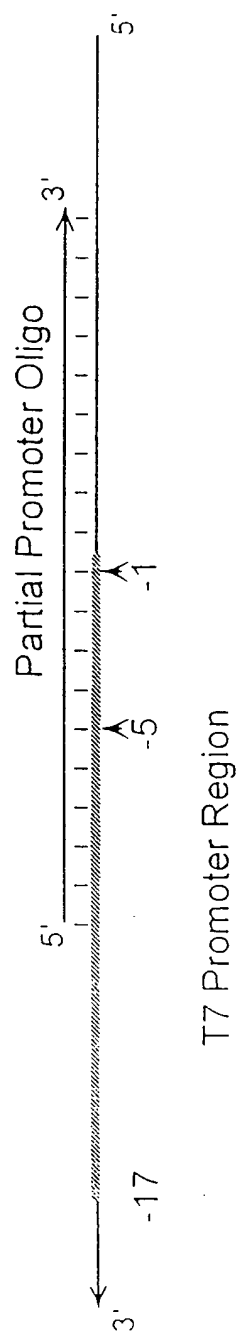


FIGURE 86B

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FIGURE 86C

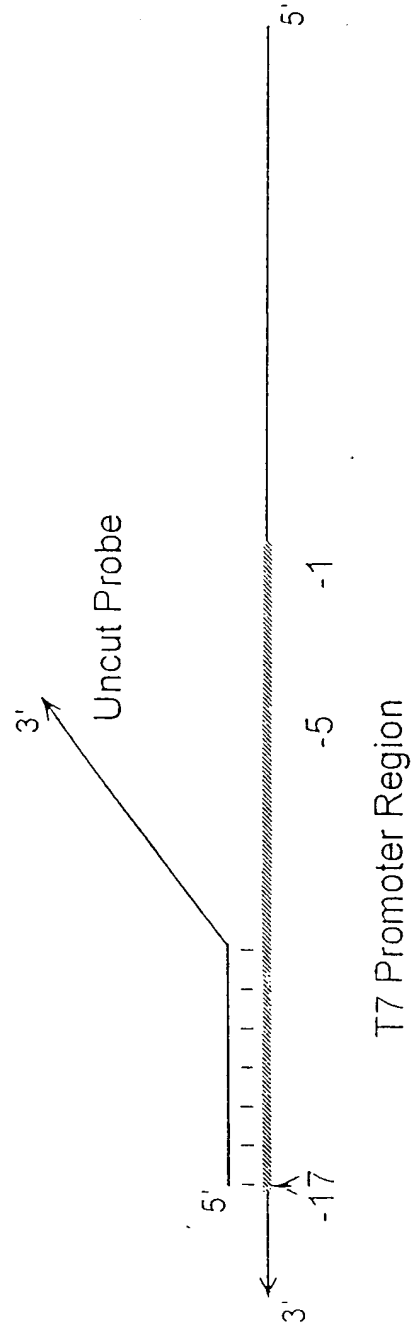
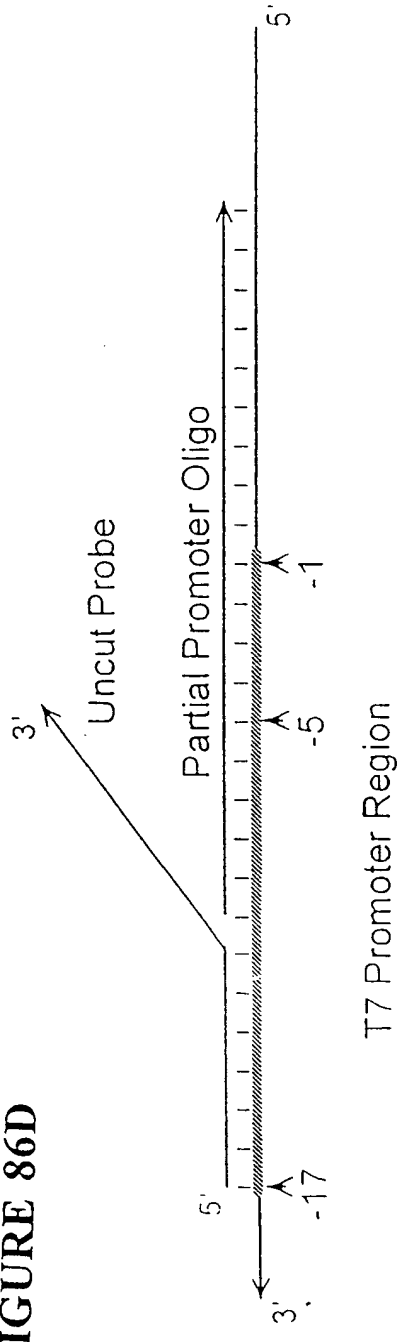
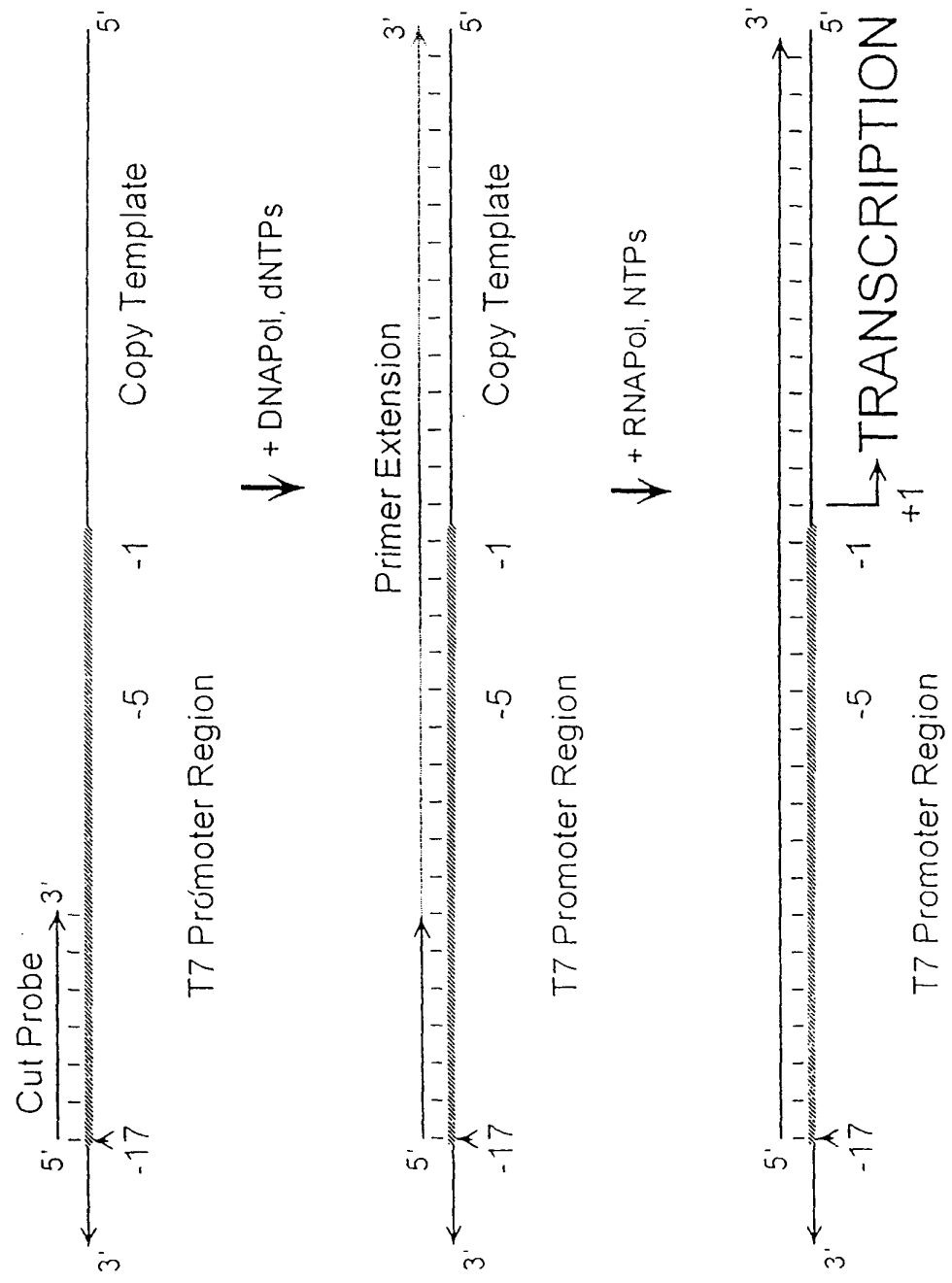


FIGURE 86D



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FIGURE 87





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FIGURE 88A

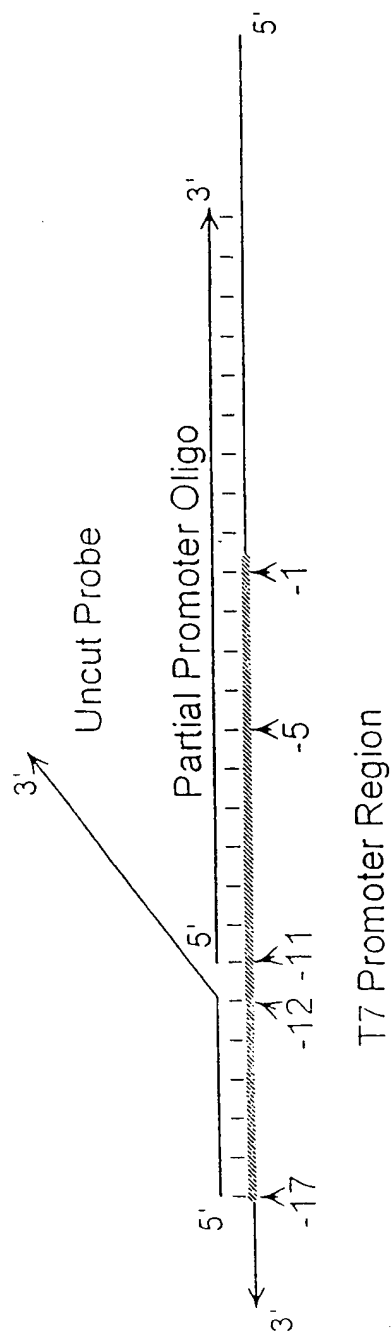


FIGURE 88B

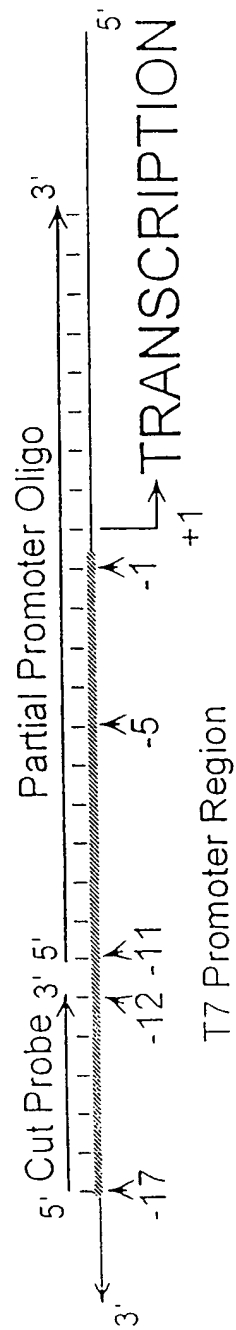
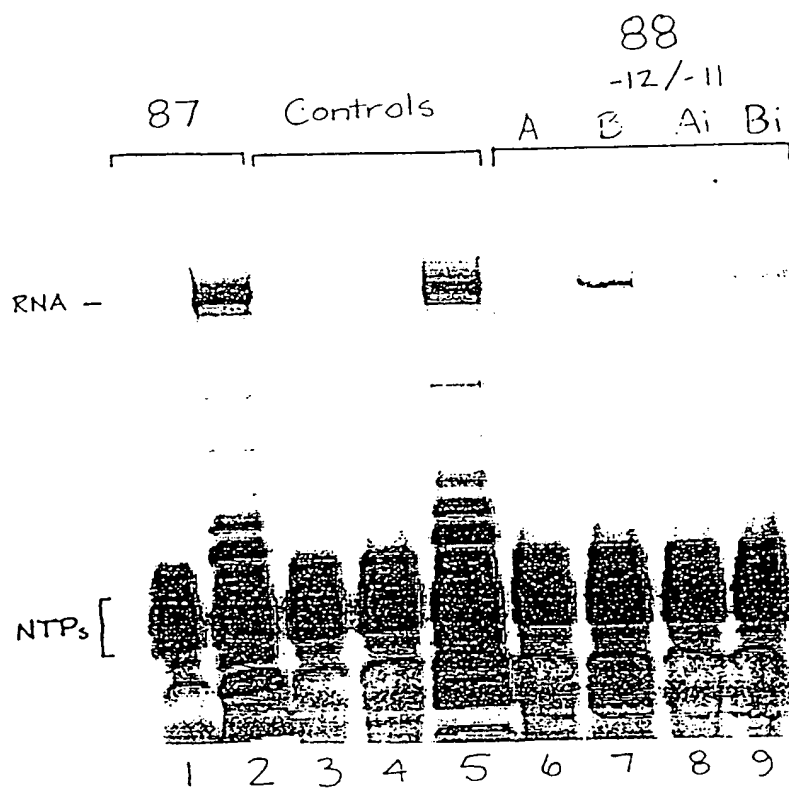


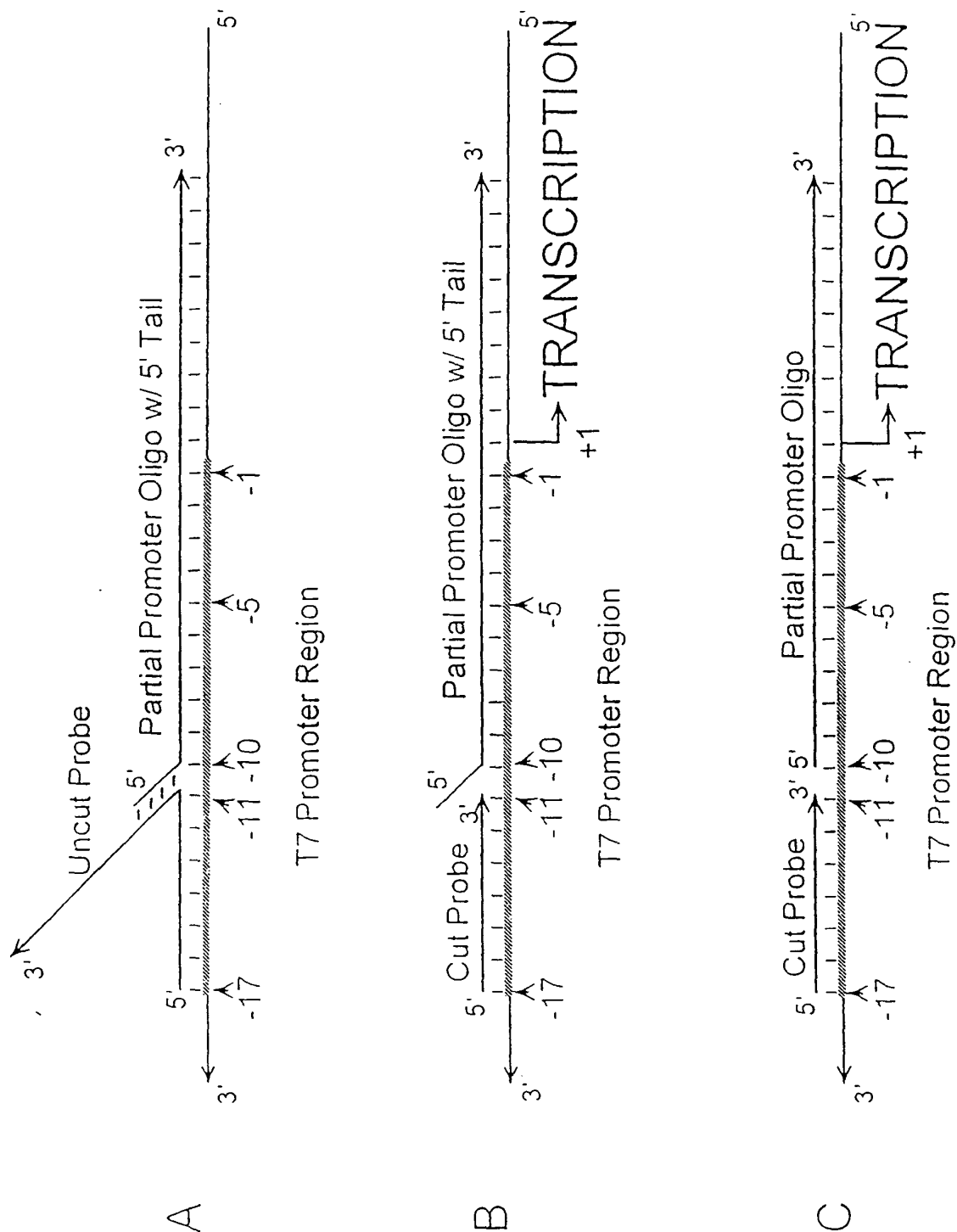
FIGURE 89



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FIGURE 90



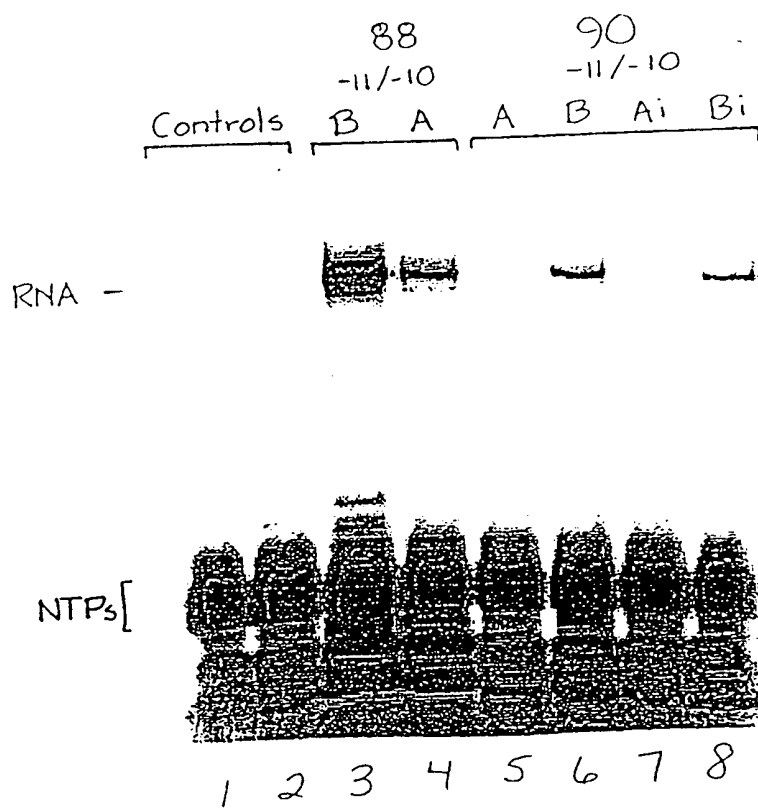
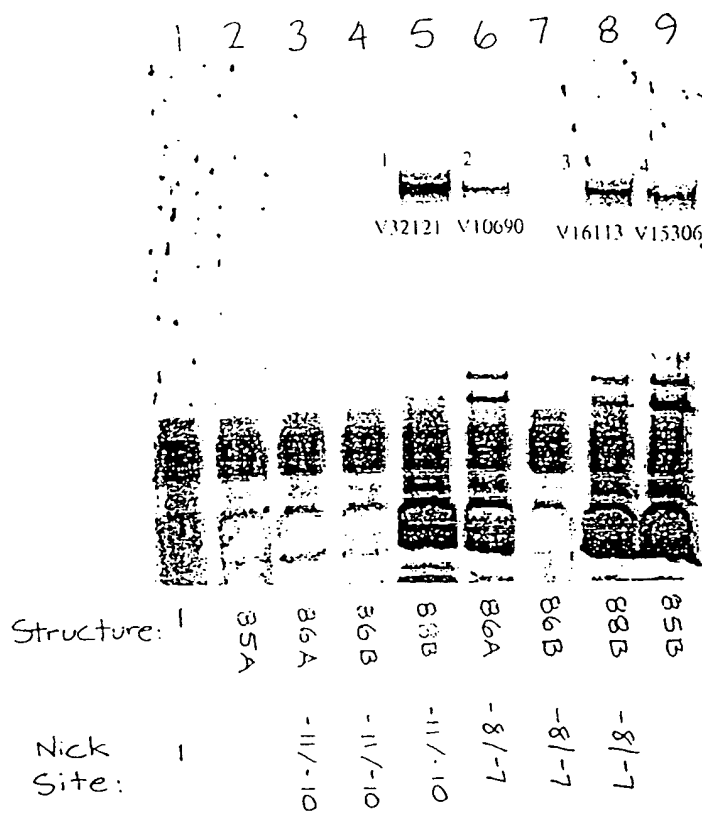


FIGURE 91

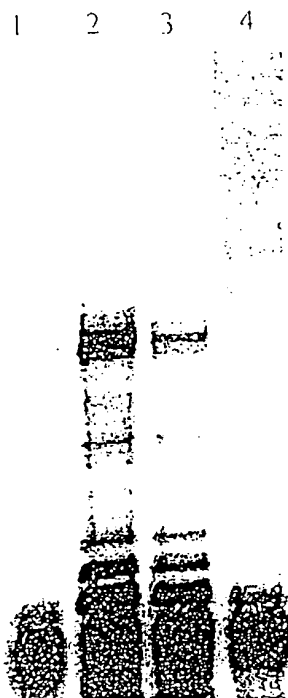
FIGURE 92



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FIGURE 93

RNA —



1  
3' - gctttaattatgctgagtqatccccagaagatacctccagttttgt - 5'  
-23 -20 -15 -10 -5 -1  
| T7 promoter region |

85A

2  
5' - cgaaattaatacgaactcactata - 3'  
3' - gctttaattatgctgagtqatccccagaagatacctccagttttgt - 5'  
-23 -20 -15 -10 -5 -1  
| T7 promoter region |

85B

3  
#073-065  
5' - cgaaattaatacgaactcactatacccagaa - 3'  
3' - gctttaattatgctgagtqatccccagaagatacctccagttttgt - 5'  
-23 -20 -15 -10 -5 -1  
| T7 promoter region |

85C

4 No DNA

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↑ TRANSCRIPTION

FIGURE 95A

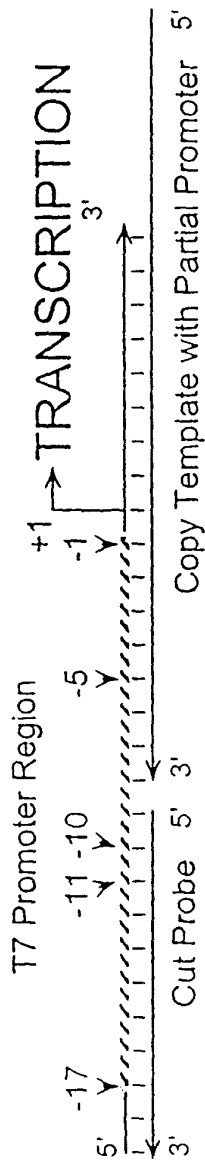


FIGURE 95B

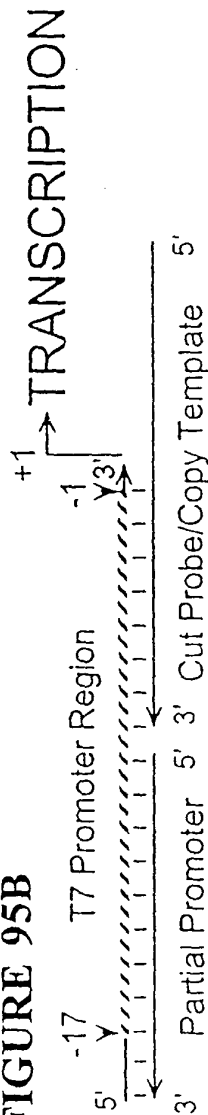


FIGURE 95C

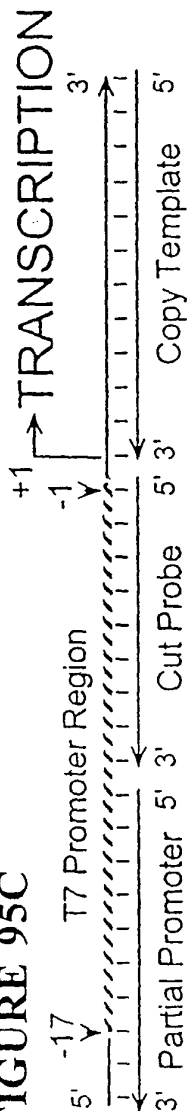
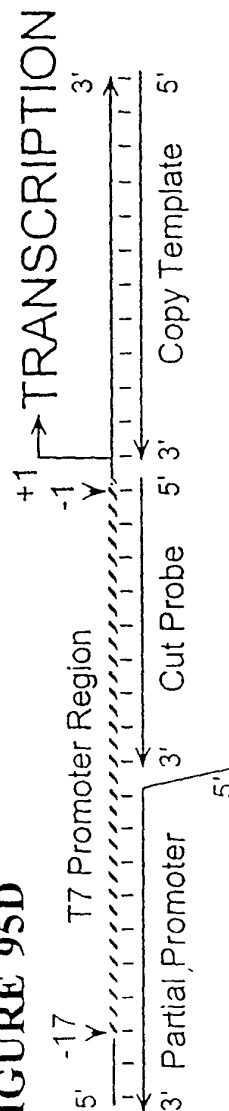


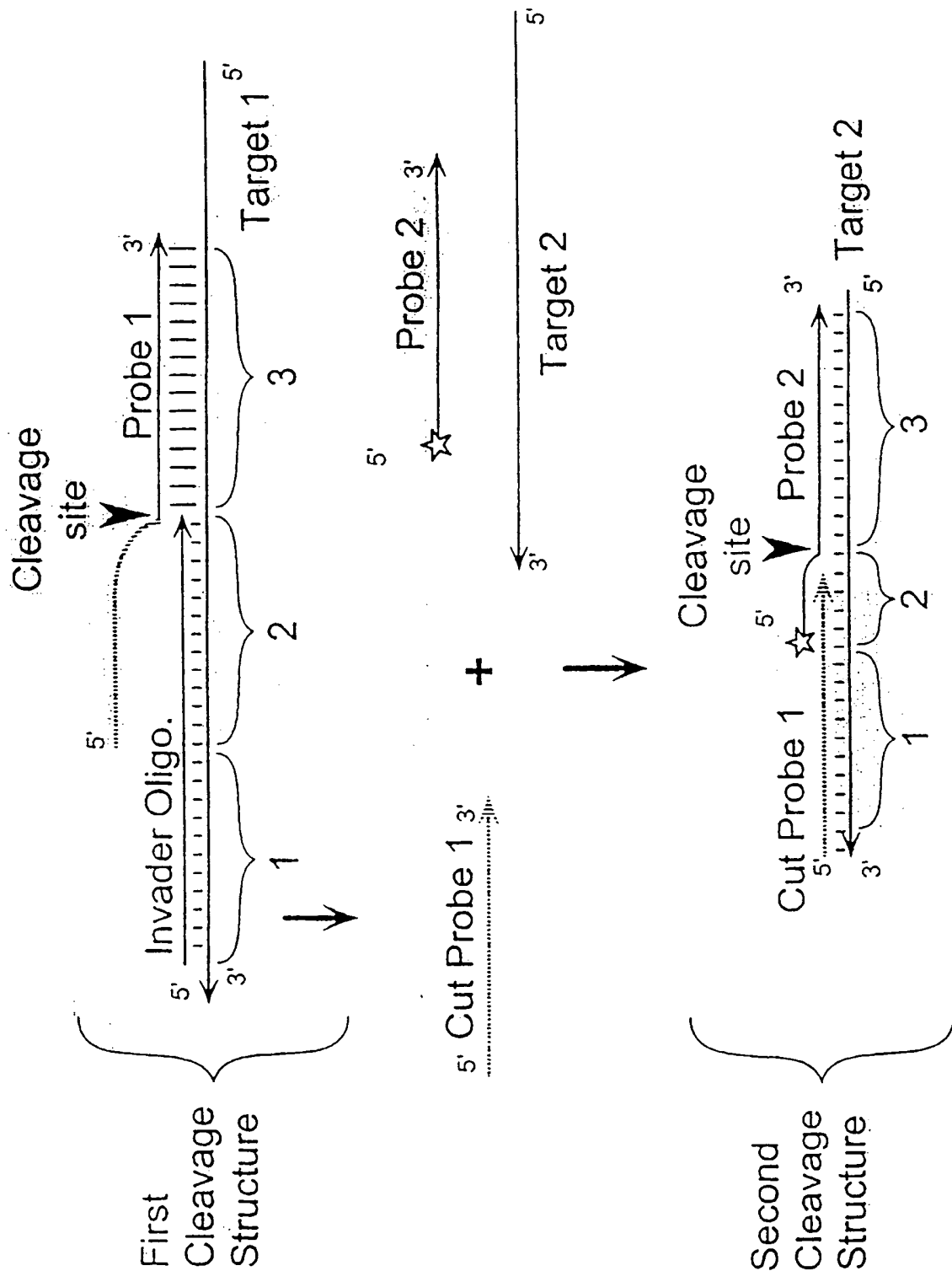
FIGURE 95D



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FIGURE 96



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FIGURE 97

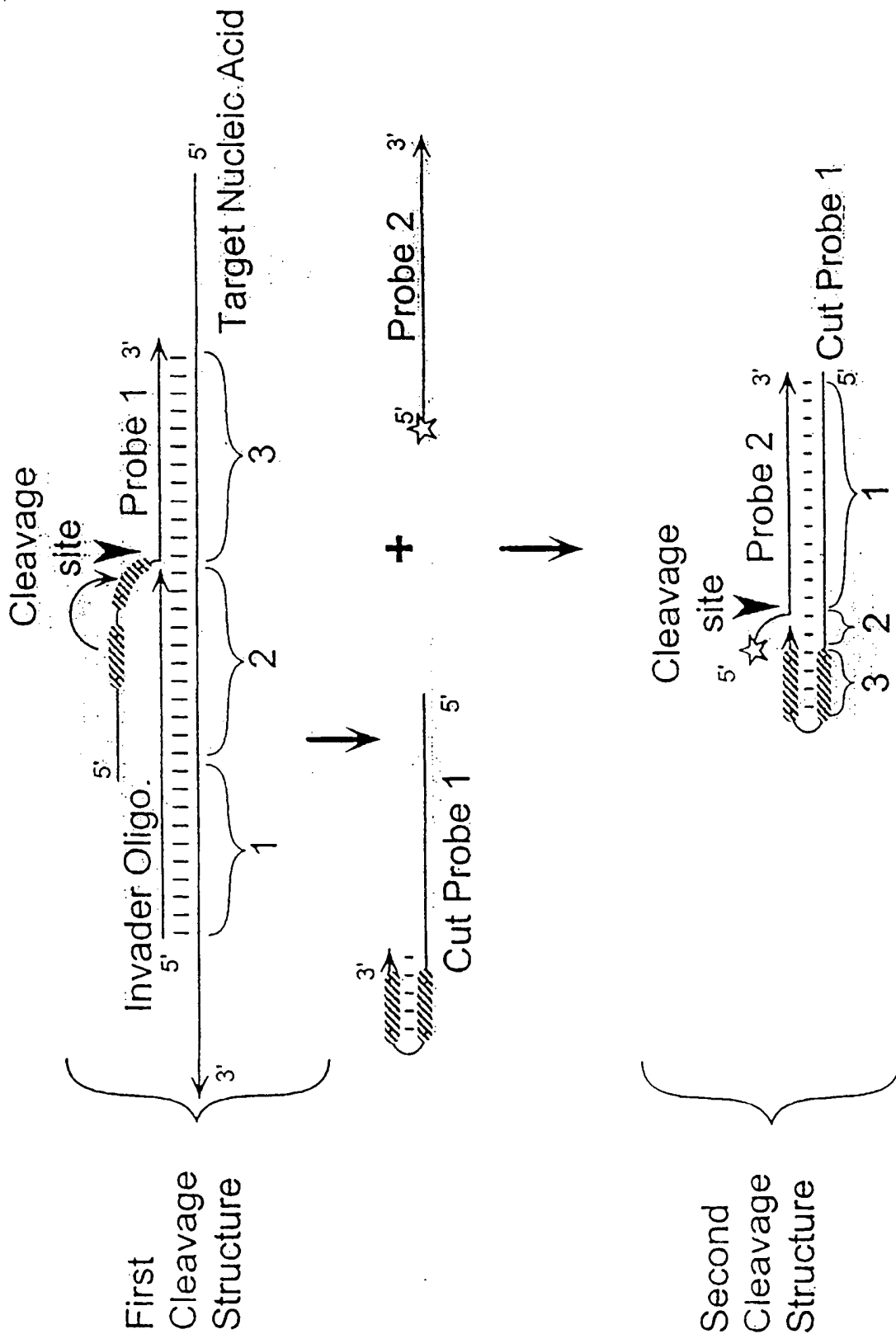


FIGURE 98

PR1 probe

Cleavage site

5'FITTTTCCAGAGCCTAAT G3'

IT3 Invader-Target

A<sup>A</sup> ACGAGCGTCTTT G3'  
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A<sup>A</sup> AGCGTCTT G3'  
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A<sup>A</sup> CGTCTT G3'  
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A<sup>A</sup> TCCTT G3'  
G AGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-3 Invader-Target

A<sup>A</sup> CTT G3'  
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

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FIGURE 99

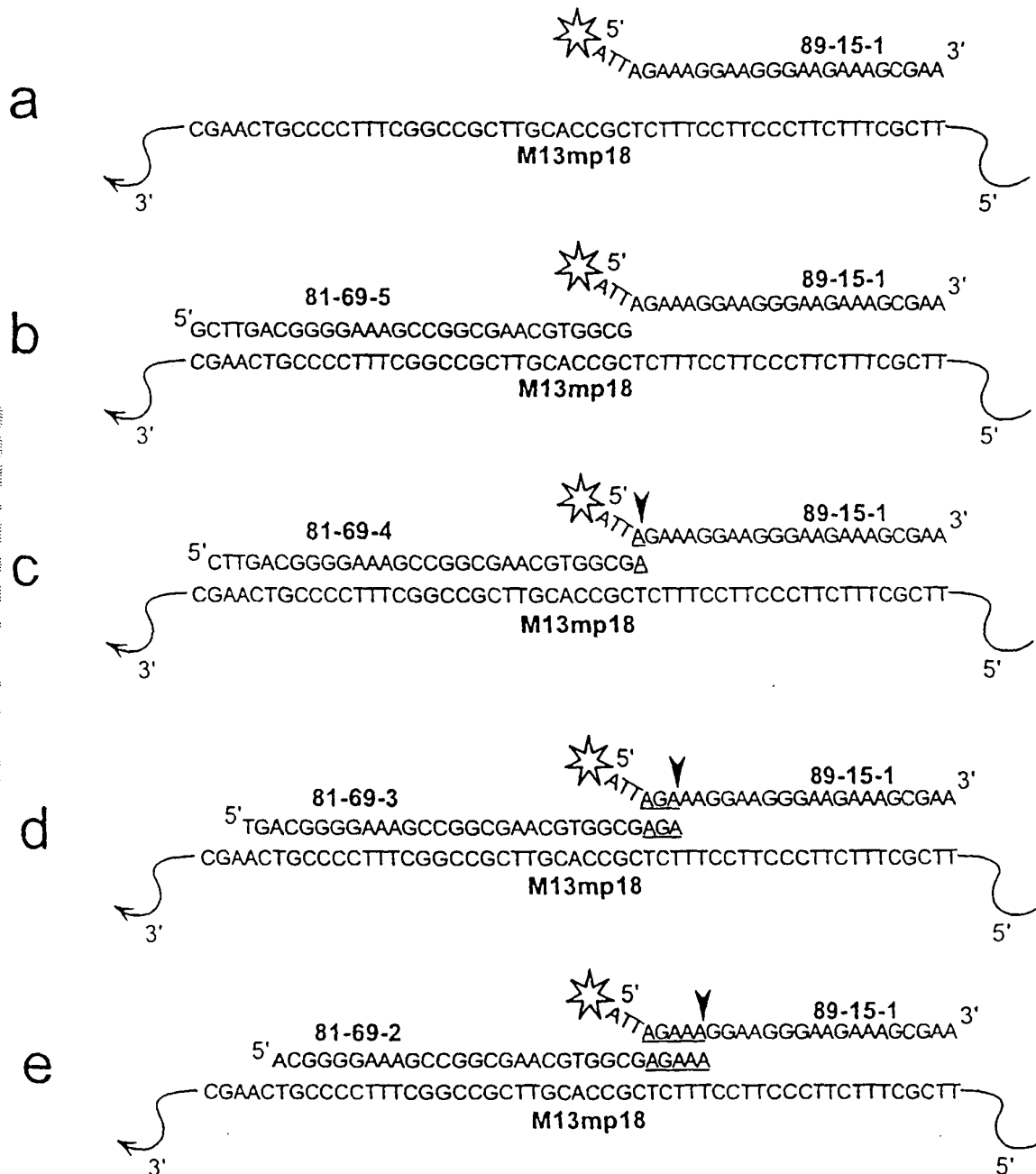
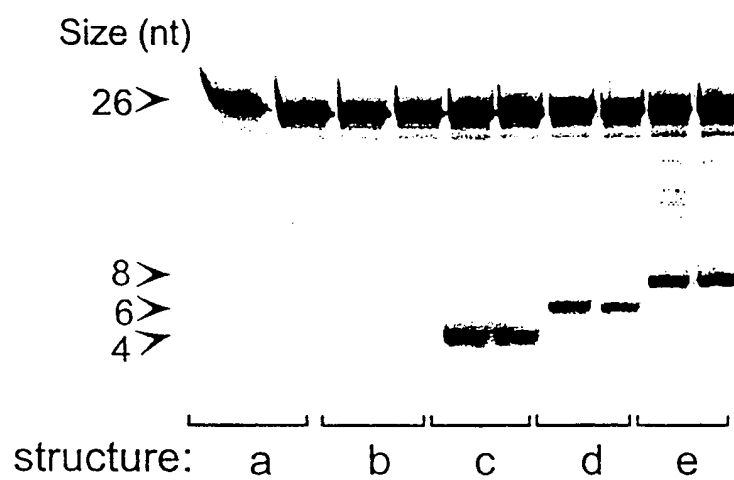


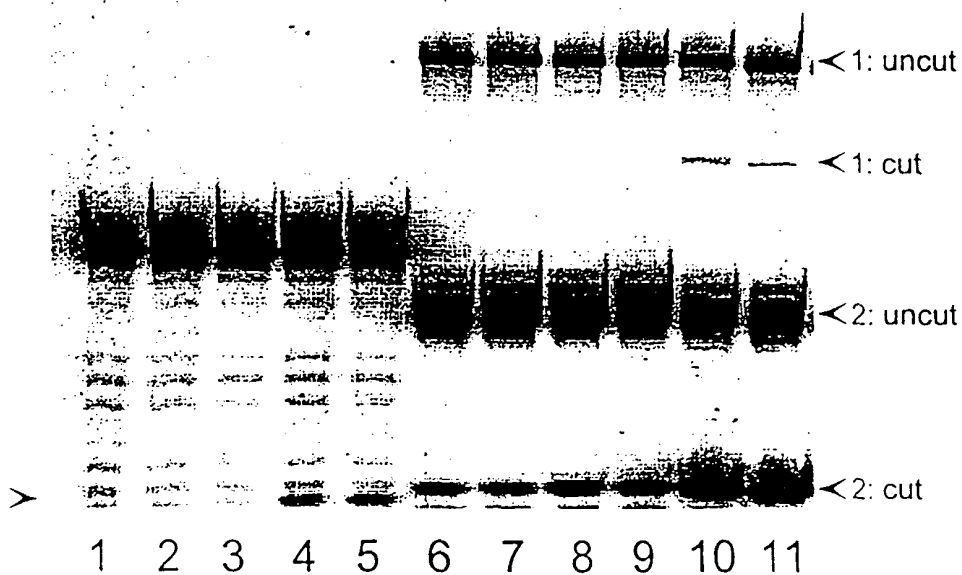
FIGURE 100



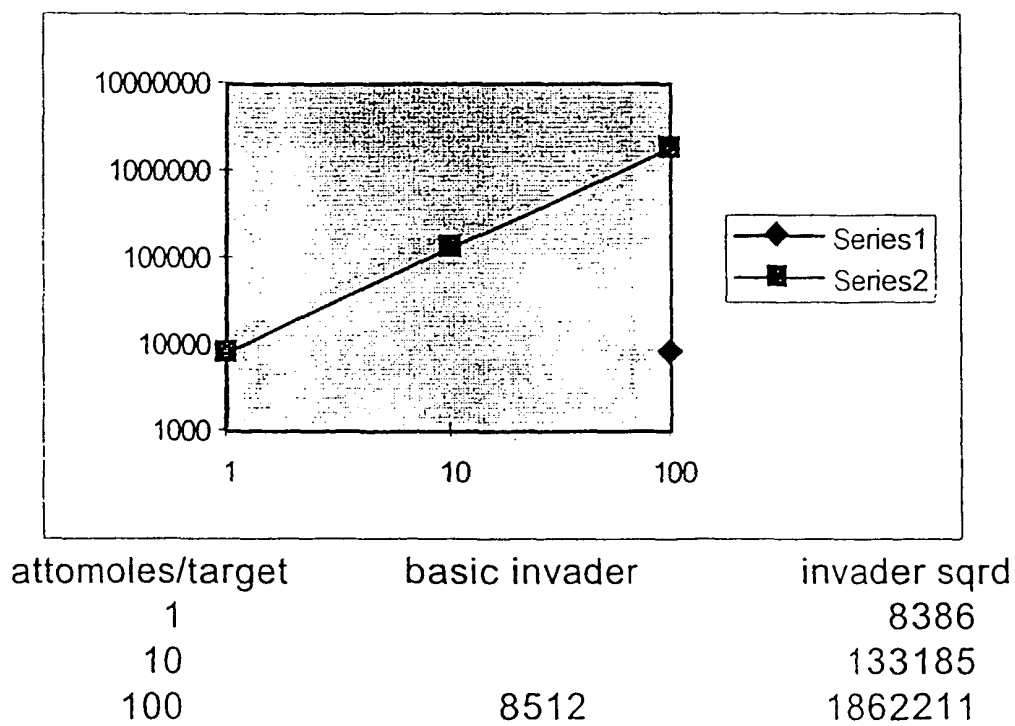
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FIGURE 101

a

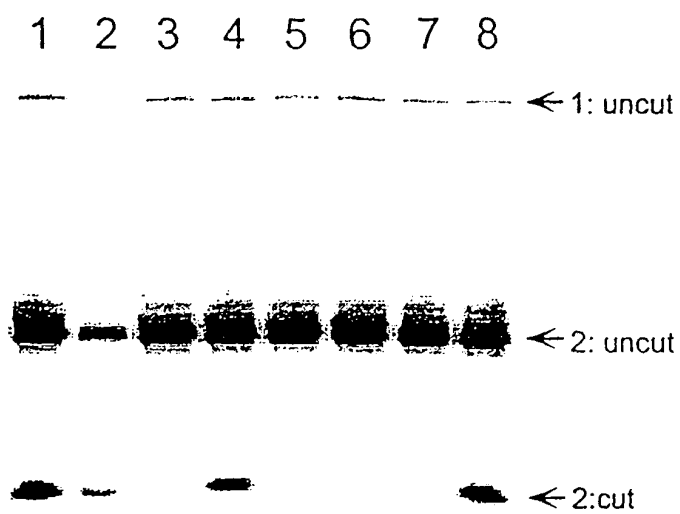


b



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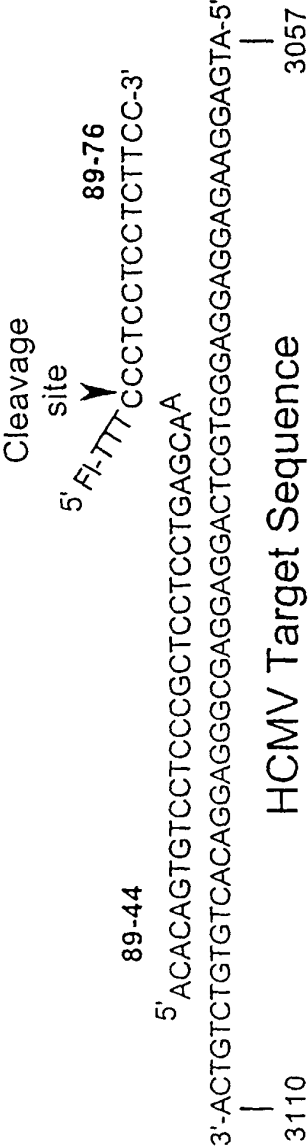
FIGURE 102



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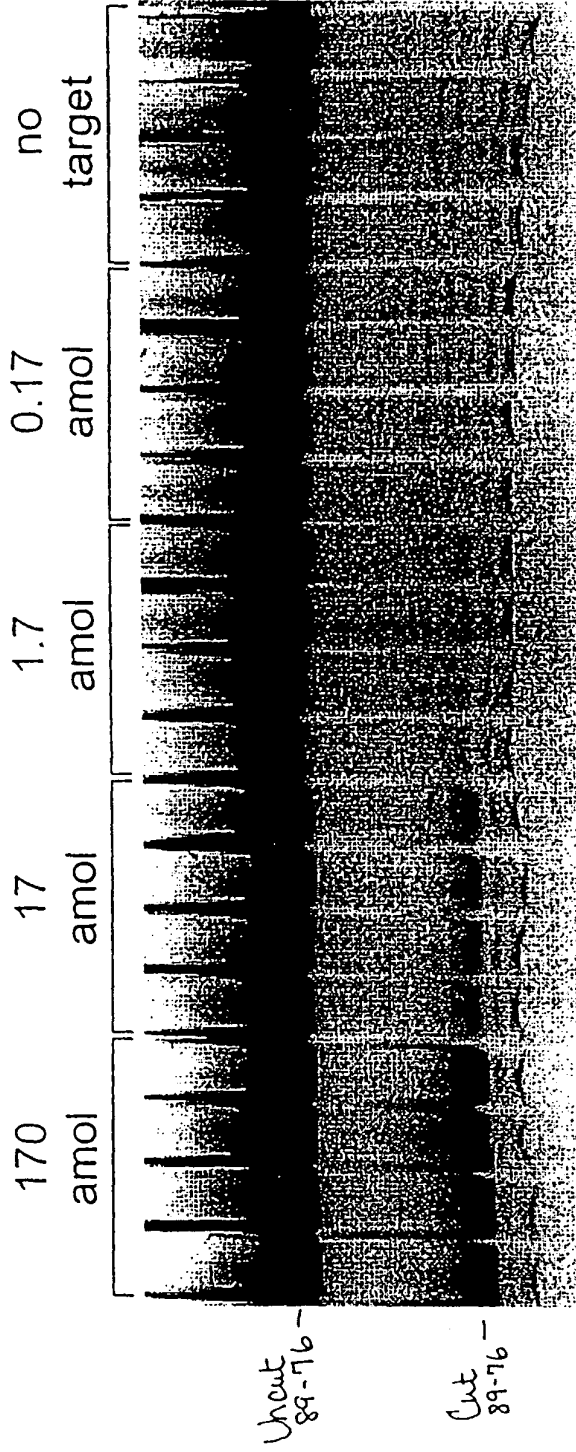
FIGURE 103





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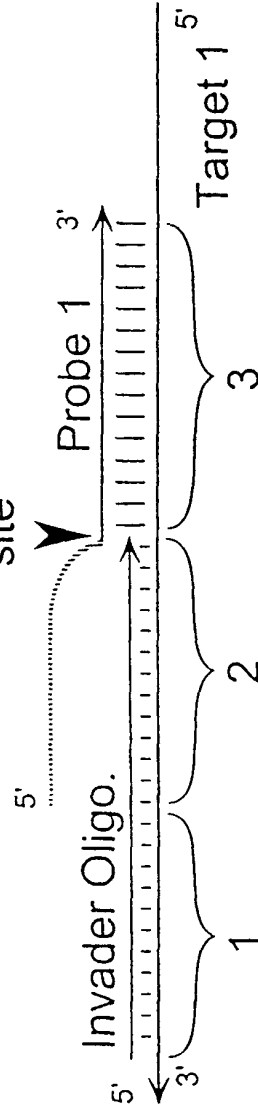
FIGURE 104



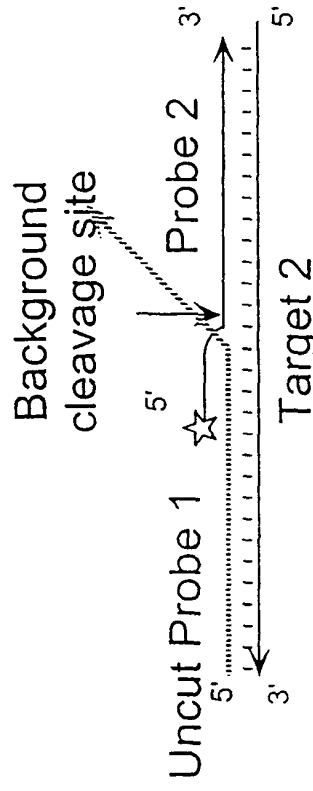
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FIGURE 105

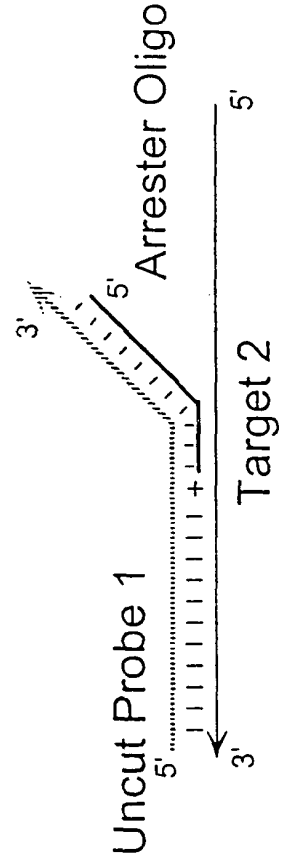
Cleavage site



Background cleavage site



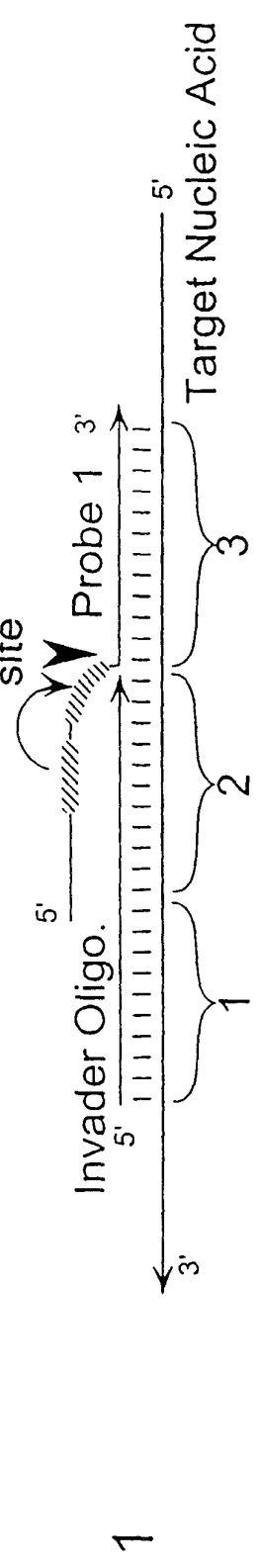
Cleavage site



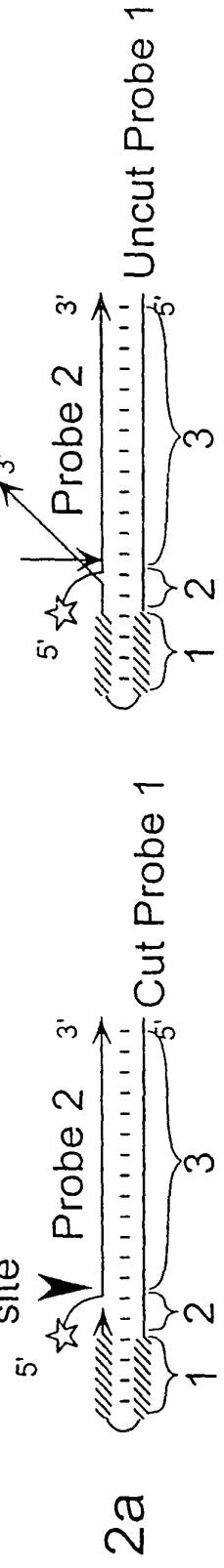
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FIGURE 106

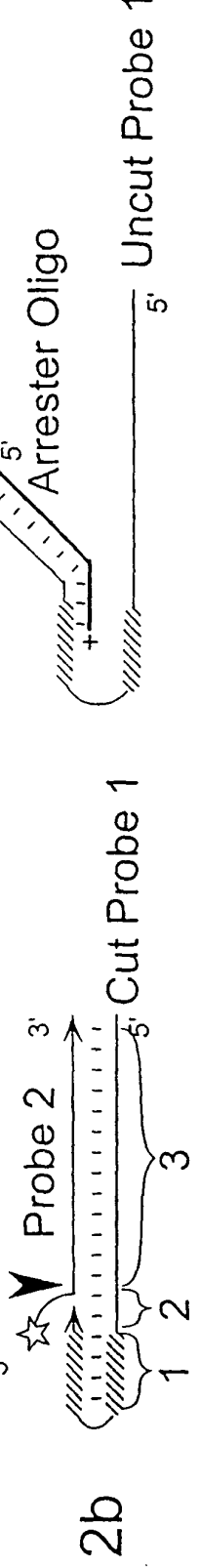
Cleavage site



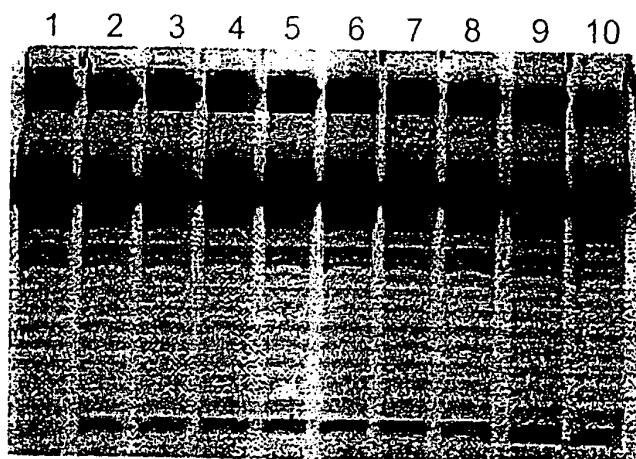
Background cleavage site



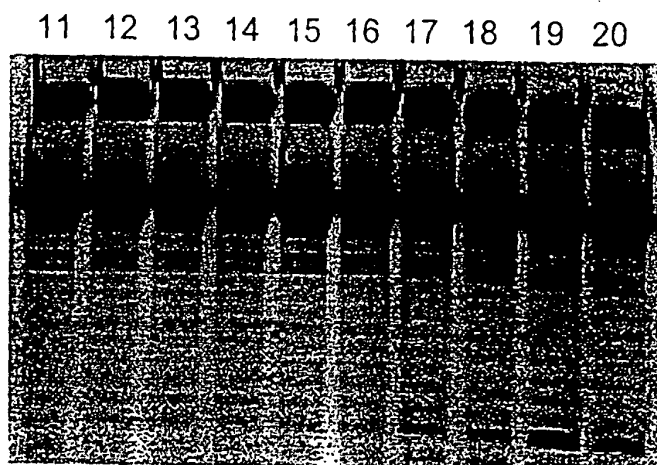
Cleavage site



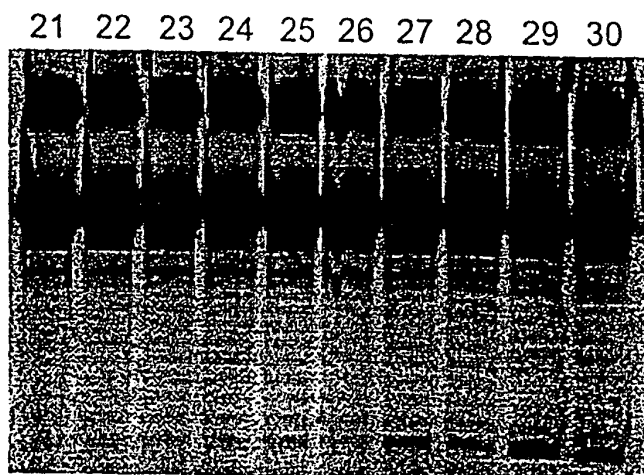
A



B



C

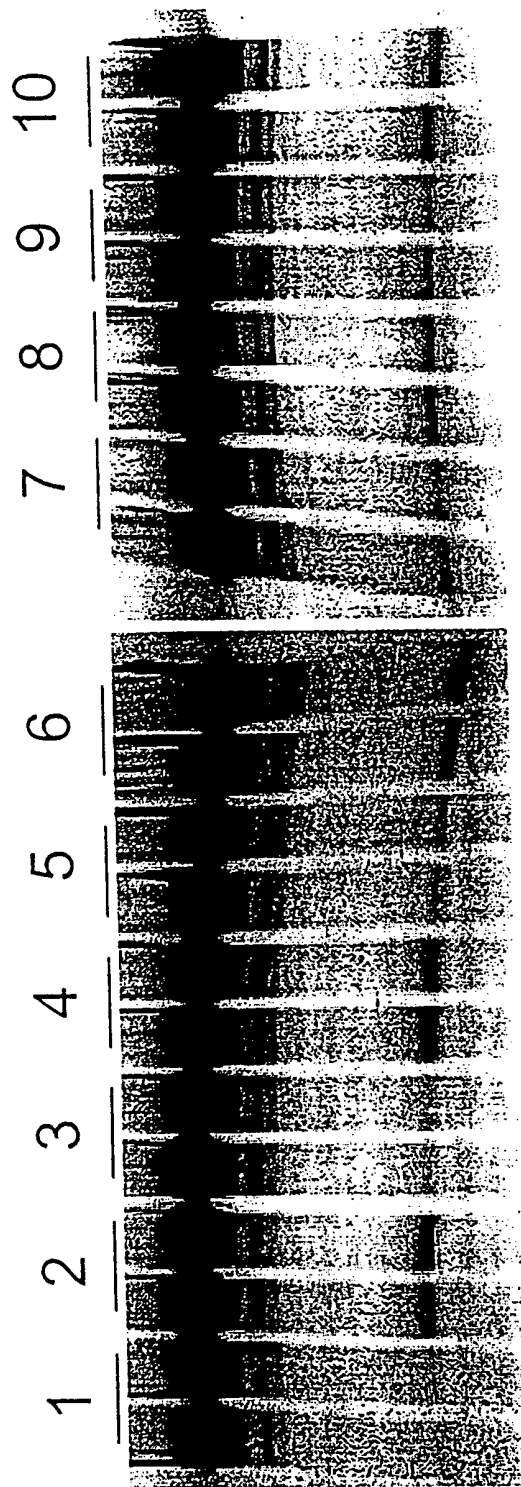


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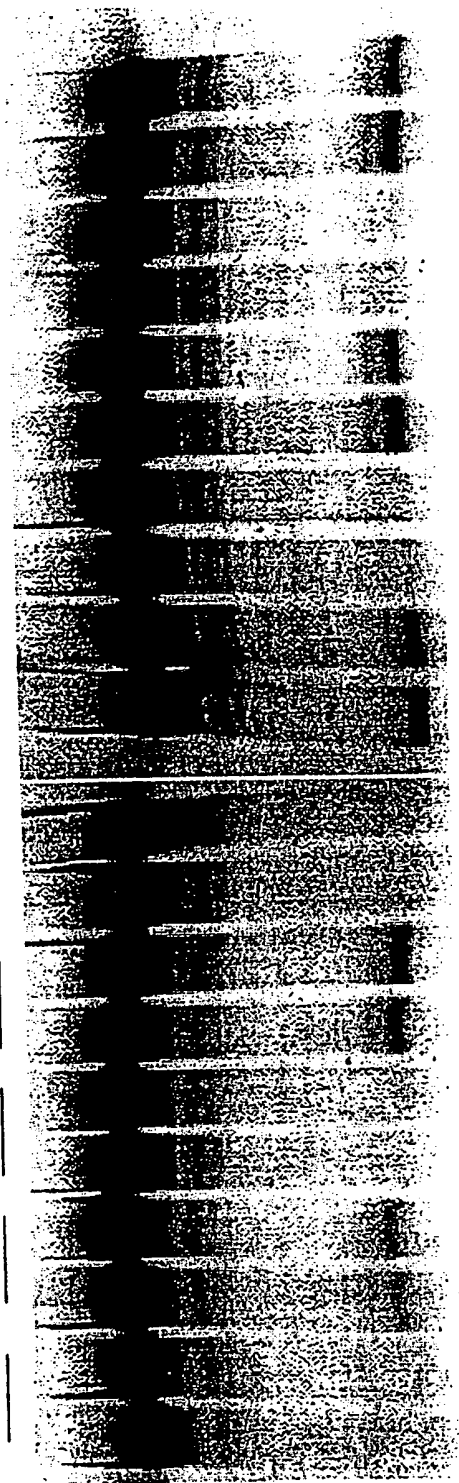
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FIGURE 108A



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- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10



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FIGURE 108C

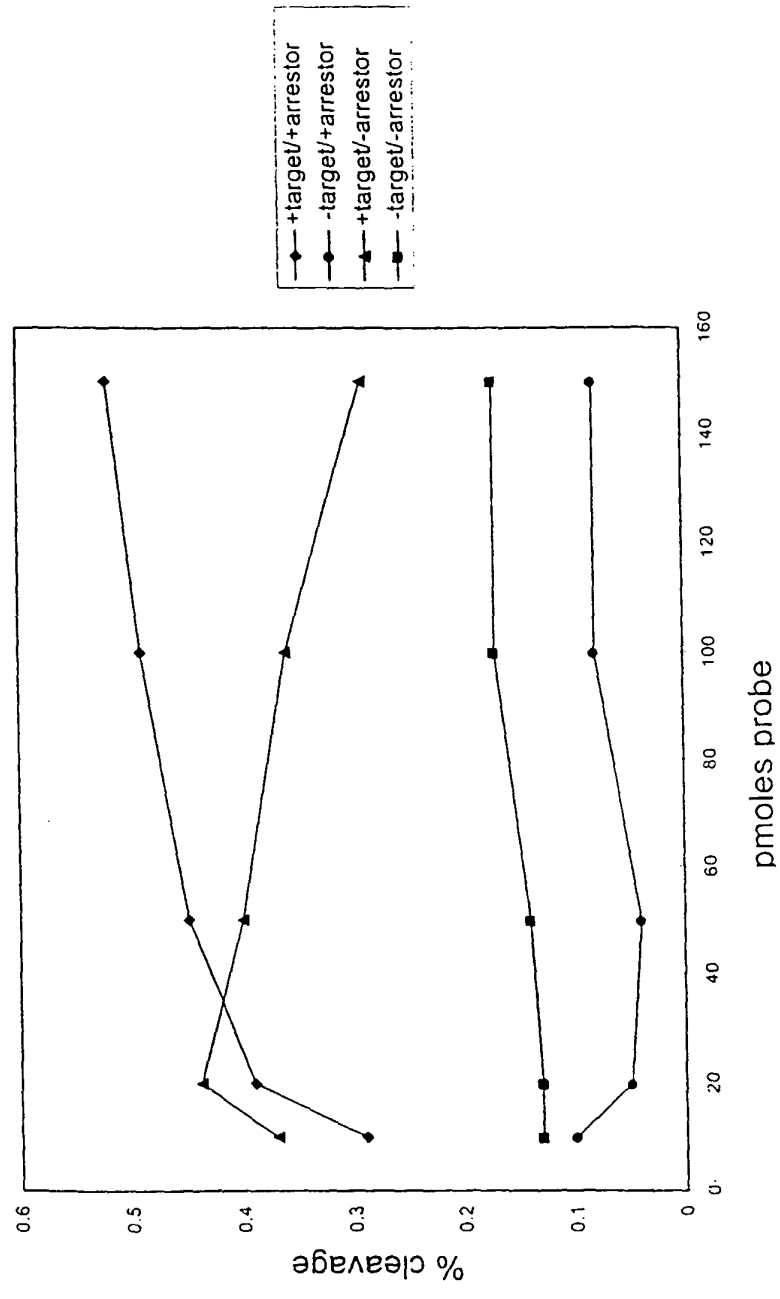
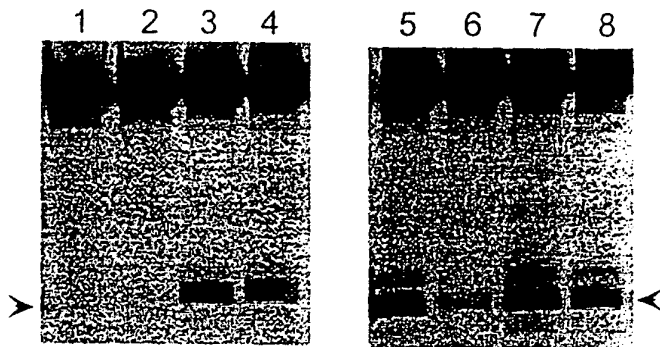


FIGURE 109A



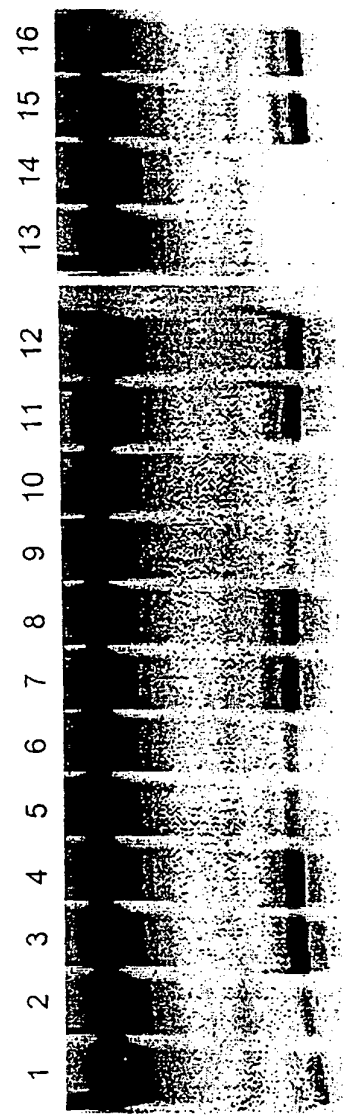
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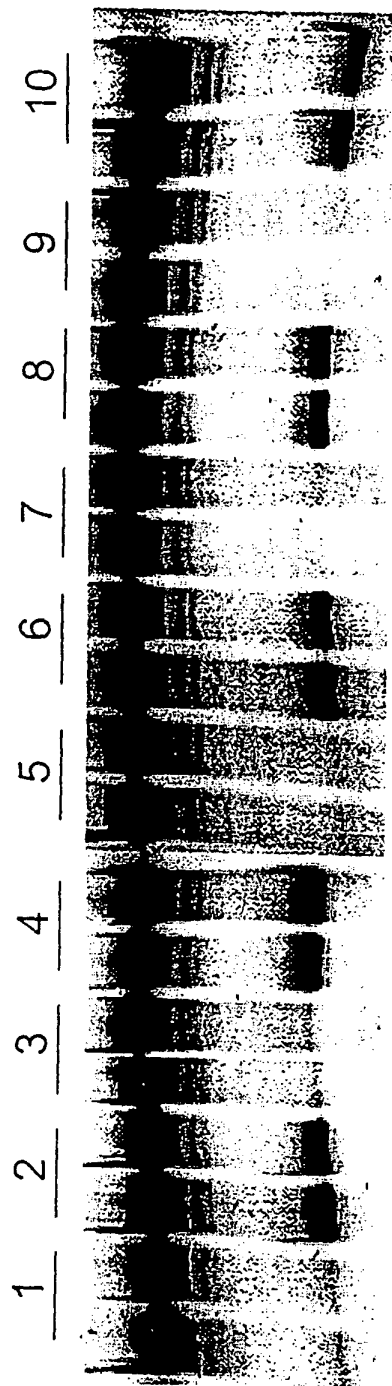
00377-70367200

FIGURE 109B



QCTT-TEST

FIGURE 110A



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DEPT. OF THE ARMY

FIGURE 110B

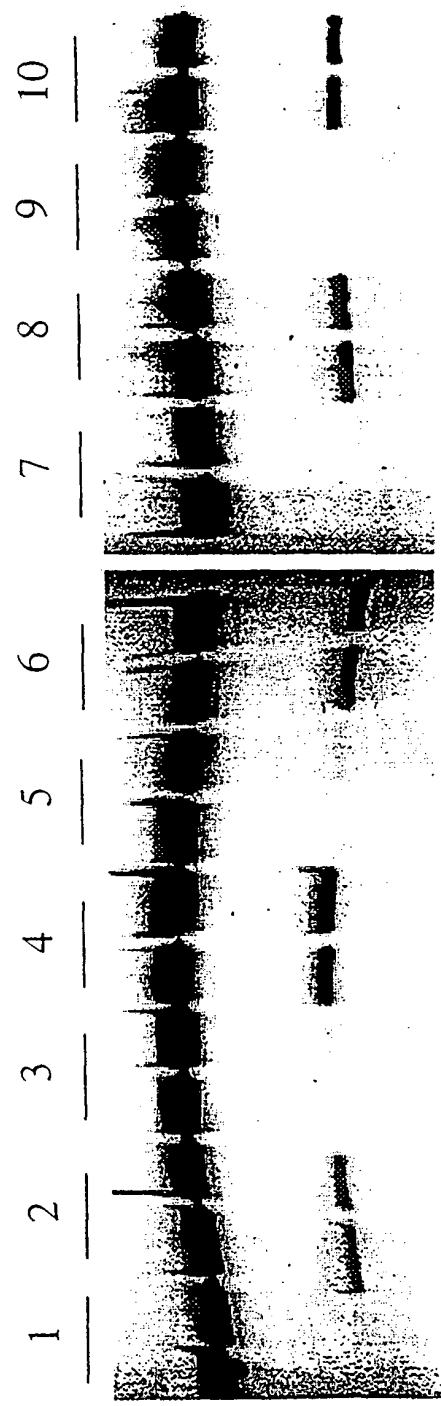
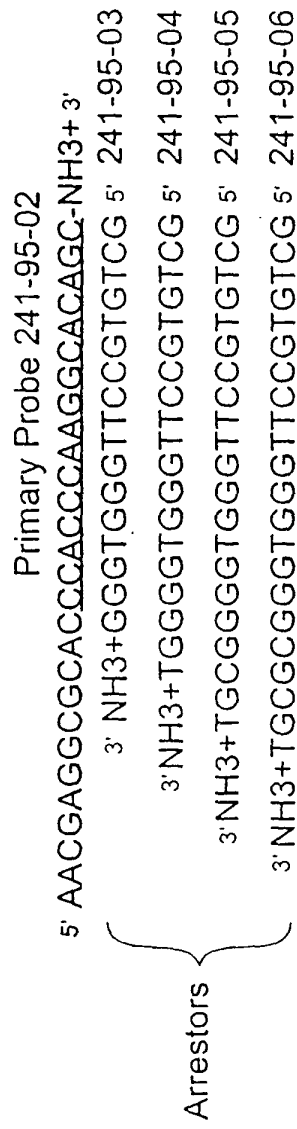


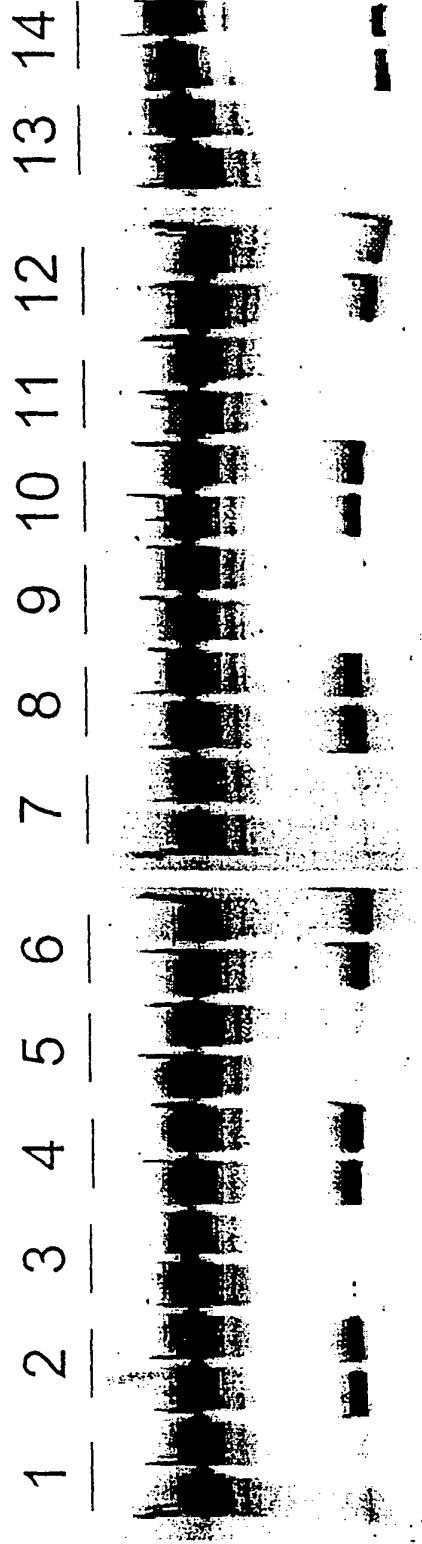
FIGURE 110C



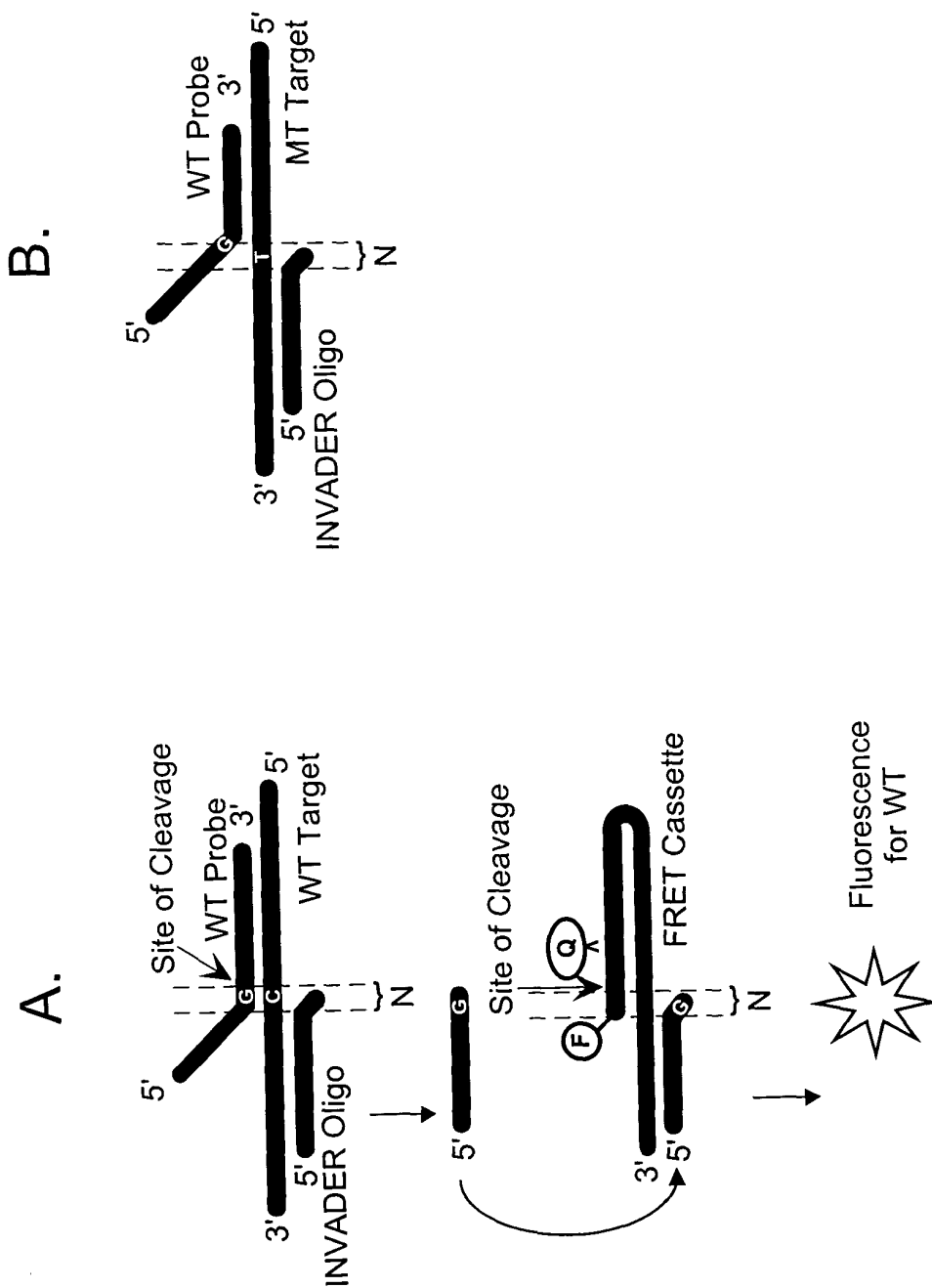
CONFIDENTIAL

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FIGURE 111



# FIGURE 112



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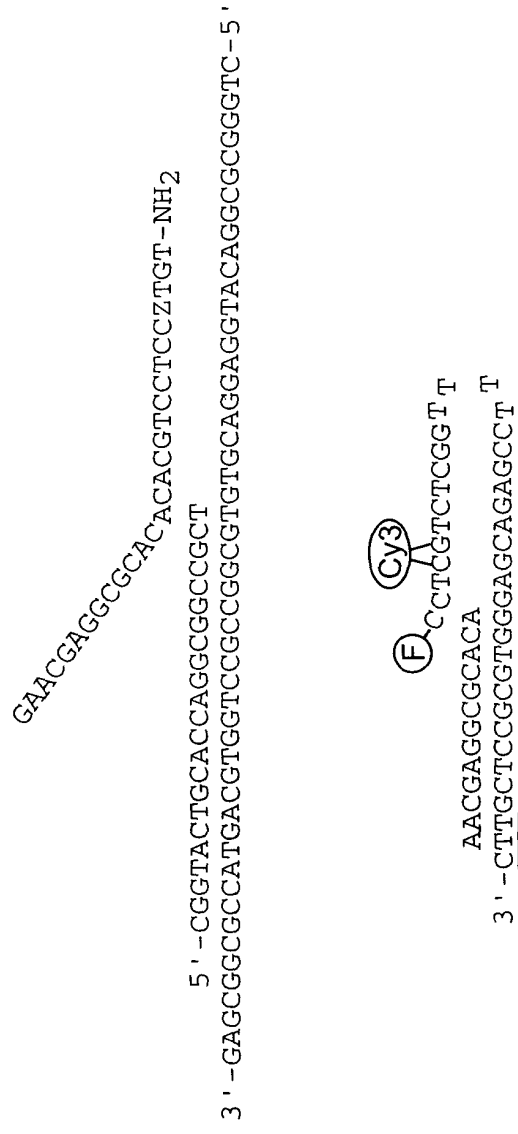
# FIGURE 113A

5'-AACGAGGCGCACGCAGTCCTCCATGT  
5'-CGGTACTGCACCAAGGCGGCGCT  
3'-GAGCGCGCCATGACGTGTCGCGCGCGGTGCAGGAGGTACAGGCGCGGGTC-5'

(F) (Cy3) CCTCTCTCGGT  
AACGAGGCGCAG  
3'-CTTGCTCCGCGTGGGAGCAGAGCCT

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# FIGURE 113B





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# FIGURE 113C

5'-AACGAGGCGCACGCTTCTGCAGGTCATC  
 5'-CCCCGGCCTGGTACACTGCCAGGCT  
 3'-AGCGCCCGGGCCGACCATGTGACGGTCCGCGAAGACGTCAGTAGCCGTAGCGC-5'

(F) (Cy3)  
 AACGAGGCGCACG  
 3'-CTTGCTCCGCGTGGGAGCAGAGCCCT

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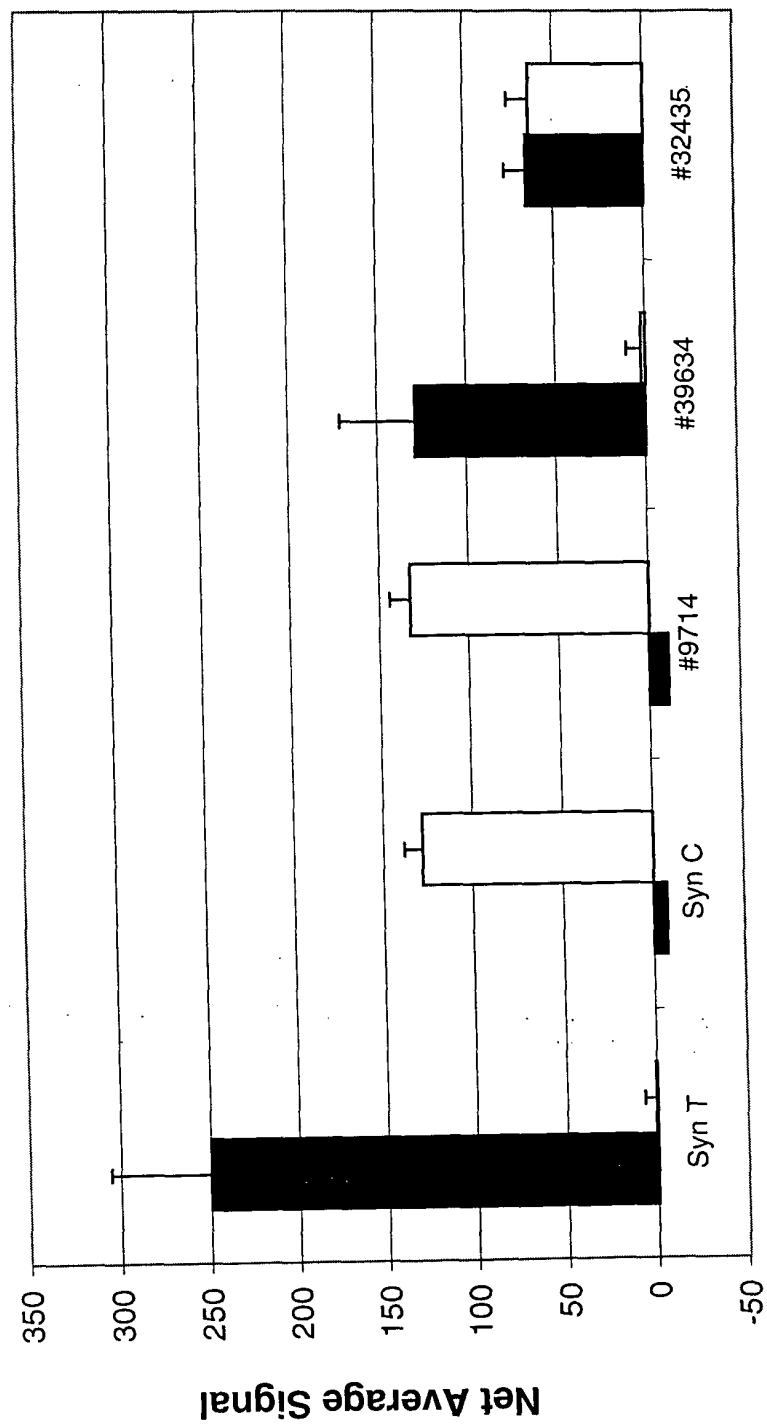
# FIGURE 113D

5'-AACGAGGCGCACACTTCTGCZGGTCATC  
5'-CCCCGGCCTGGTACACTGCCAGGCT  
3'-AGCGCCCGGGCCGACCATGTGACGGTCCGTGAAGACGTCCAGTAGCCGTAGCGC-5'

(Cy3)  
(F) C CTCGTCTCGGT T  
AACGAGGCGCACA  
3'-CTTGCTCCCGCTGGGAGCAGAGCCCT T

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FIGURE 114A



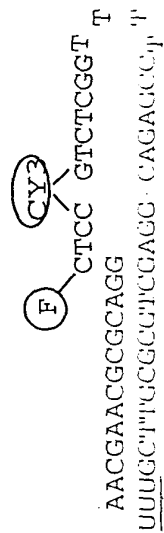
1	100	100%
2	100	100%
3	100	100%
4	100	100%
5	100	100%
6	100	100%
7	100	100%
8	100	100%
9	100	100%
10	100	100%
11	100	100%
12	100	100%
13	100	100%
14	100	100%
15	100	100%
16	100	100%
17	100	100%
18	100	100%
19	100	100%
20	100	100%
21	100	100%
22	100	100%
23	100	100%
24	100	100%
25	100	100%
26	100	100%
27	100	100%
28	100	100%
29	100	100%
30	100	100%
31	100	100%
32	100	100%
33	100	100%
34	100	100%
35	100	100%
36	100	100%
37	100	100%
38	100	100%
39	100	100%
40	100	100%
41	100	100%
42	100	100%
43	100	100%
44	100	100%
45	100	100%
46	100	100%
47	100	100%
48	100	100%
49	100	100%
50	100	100%
51	100	100%
52	100	100%
53	100	100%
54	100	100%
55	100	100%
56	100	100%
57	100	100%
58	100	100%
59	100	100%
60	100	100%
61	100	100%
62	100	100%
63	100	100%
64	100	100%
65	100	100%
66	100	100%
67	100	100%
68	100	100%
69	100	100%
70	100	100%
71	100	100%
72	100	100%
73	100	100%
74	100	100%
75	100	100%
76	100	100%
77	100	100%
78	100	100%
79	100	100%
80	100	100%
81	100	100%
82	100	100%
83	100	100%
84	100	100%
85	100	100%
86	100	100%
87	100	100%
88	100	100%
89	100	100%
90	100	100%
91	100	100%
92	100	100%
93	100	100%
94	100	100%
95	100	100%
96	100	100%
97	100	100%
98	100	100%
99	100	100%
100	100	100%

Stimulus	Net Average Signal (approx.)	Bar Style
Syn C	-280	White
Syn T	-340	Black
31071	450	White
511	200	White
511	200	Black
537	450	White
538	200	White
538	200	Black
539	450	White

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# FIGURE 115A

5'-AACGAACGGCAGGCCAGGTGGAGCATTT-3'  
5'-CCCCGTGGGAAGAGCAGAGATATACGTC  
3'-GACCCCTTCTCGTCTCTATATGCACGGTCCACCTCGTGG-5'



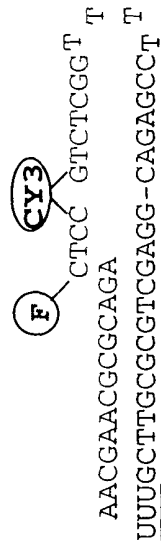
5' - A C G A A C G C G C A G A C C A G G T G G A G C A C - 3'

# FIGURE 115B

5' - A C G A A C G C G C A G A C C A G G T G G A G C A C - 3'

5' - C C C C T G G G A A G A G A G A G A T A T A C G T C

3' - G A C C C C T T C T C G T C T A T A T G C A T G G T C C A C C T C G T G G - 5'

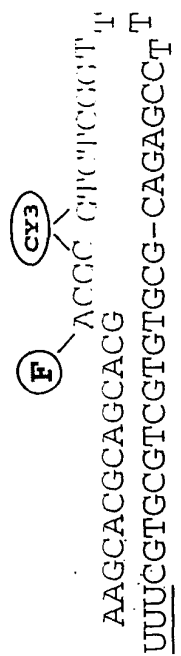


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Country	Year	Population (millions)	GDP (billion USD)	Urban population (%)	Life expectancy (years)	Infant mortality (per 1,000 live births)	Health expenditure (billion USD)	Health expenditure (% of GDP)
Algeria	2000	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2001	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2002	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2003	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2004	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2005	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2006	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2007	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2008	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2009	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2010	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2011	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2012	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2013	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2014	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2015	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2016	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2017	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2018	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2019	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2020	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2021	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2022	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2023	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2024	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2025	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2026	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2027	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2028	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2029	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2030	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2031	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2032	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2033	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2034	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2035	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2036	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2037	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2038	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2039	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2040	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2041	29.0	10.0	54.0	72.0	10.0	0.5	0.5%
Algeria	2042	29.0</						

## FIGURE 115C

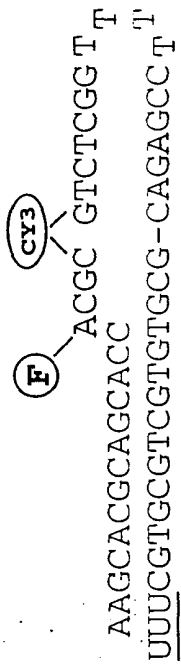
5' -AAGCAGCGAGCACGATCATAGAACACGAAACAGTTT-3'  
5' -GGGCTCCACACGGCGACTCTCATTT  
3' -GCCCCGAGGTGTCCCGCTGAGAGTACTAGTATCTTGTGCTTGTCCGA-5'



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# FIGURE 115D

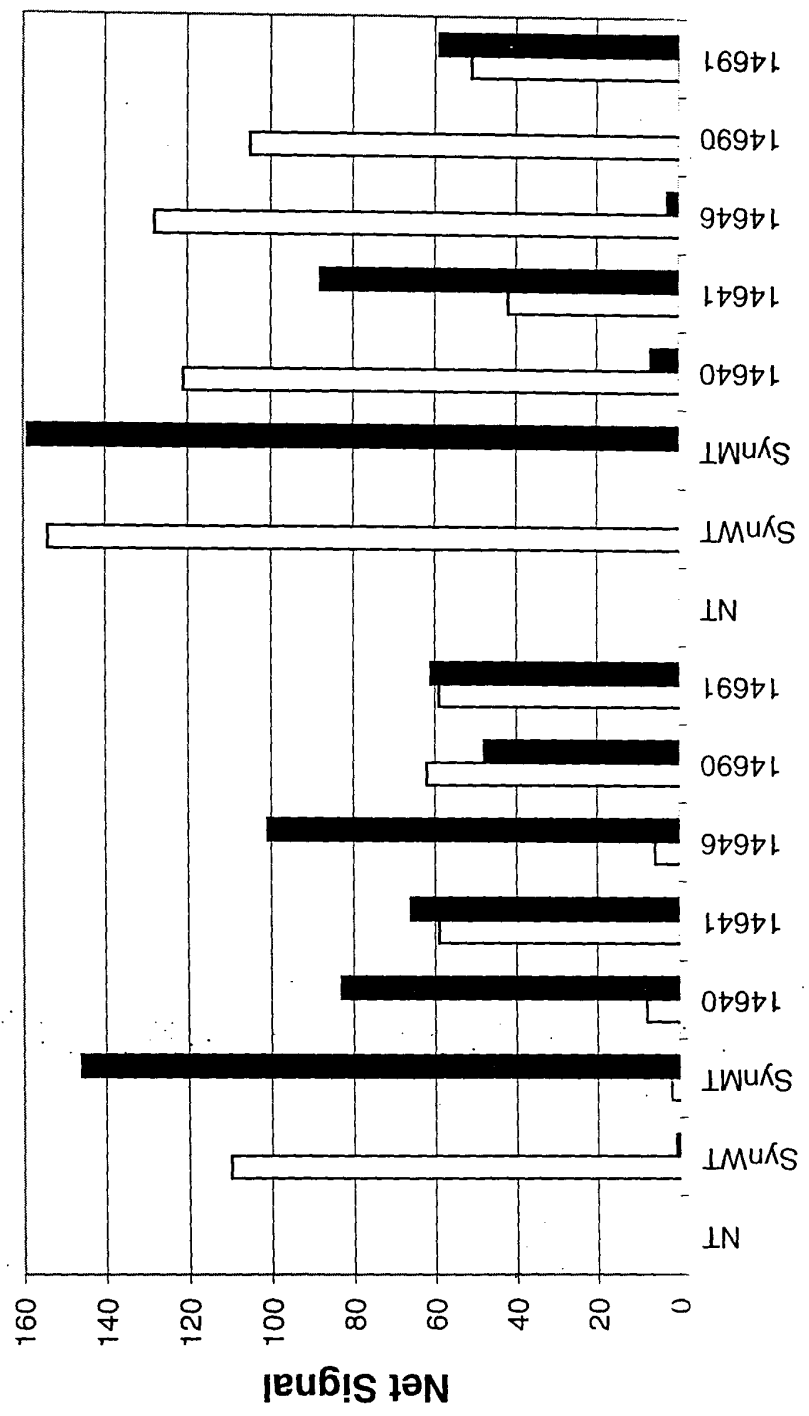
5'-AAGCAGCAGCACCATCATAGAACACGAACAGTTT-3'  
5'-GGGCTCCACACGGCGACTCTCATTT  
3'-GCCCCGAGGTGTGCCGCTGAGAGTAGTAGTATCTTGTGCTTGTCCGA-5'





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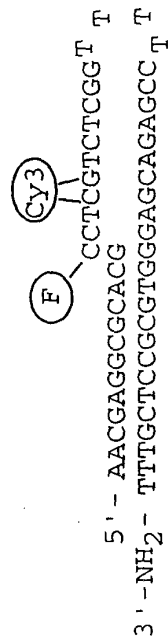
FIGURE 116



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# FIGURE 117A

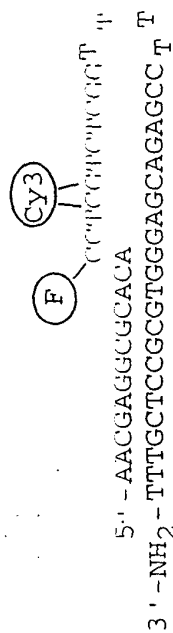
5'-AACGAGCGGCACGCTCCCGCAGACAC-3'  
5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC  
3'-GGAGTTCTTTTCGACGCACTACTTtagccgagggcgctgtggaag-5'



sa/eth

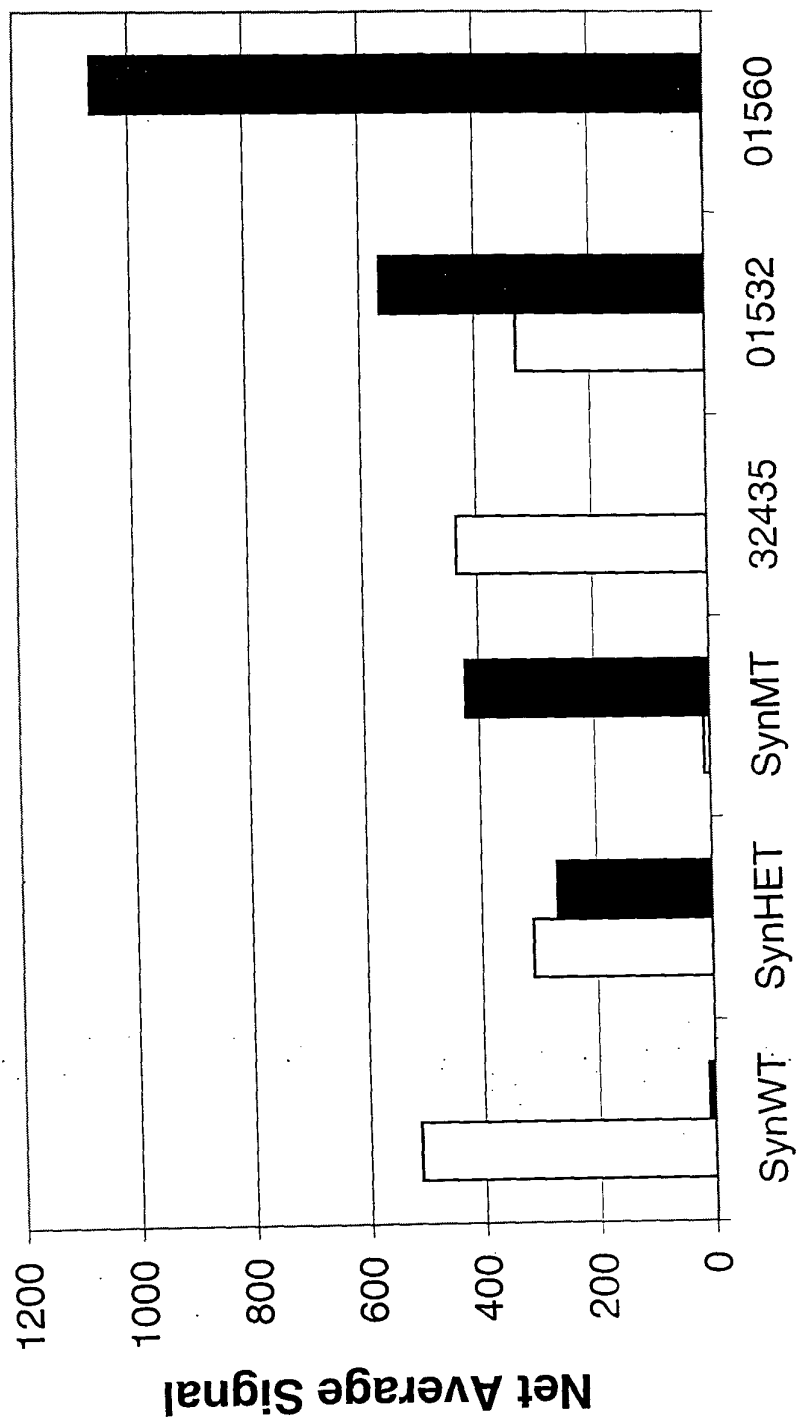
## FIGURE 117B

5'-AACGAGGCGCACTCCCGCAGACACC-3'  
5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC  
3'-GGAGTTCTTTTCGACGCACTACTTAGCTGAGGGCGTCTGTGGAAG-5'



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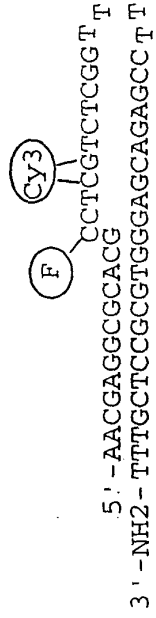
Genotype	Net Average Signal (White Bar)	Net Average Signal (Black Bar)
SynWT	~500	~10
SynHET	~300	~250
SynMT	~10	~450
32435	~450	0
01532	~450	~550
01560	0	~1100



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# FIGURE 119A

5'-AACGAGGCGCACGAGCCTCAATGCTCCC-NH2-3'  
5'-TATGGTTCCCAATAAAAGTGACTCTCAGCT  
3'-TTGATACCAAGGTTATTTTCACTGAGAGTCGCTCGGAGTTACGAGGGTCA-5'



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5'-AACGAGGCGCAC

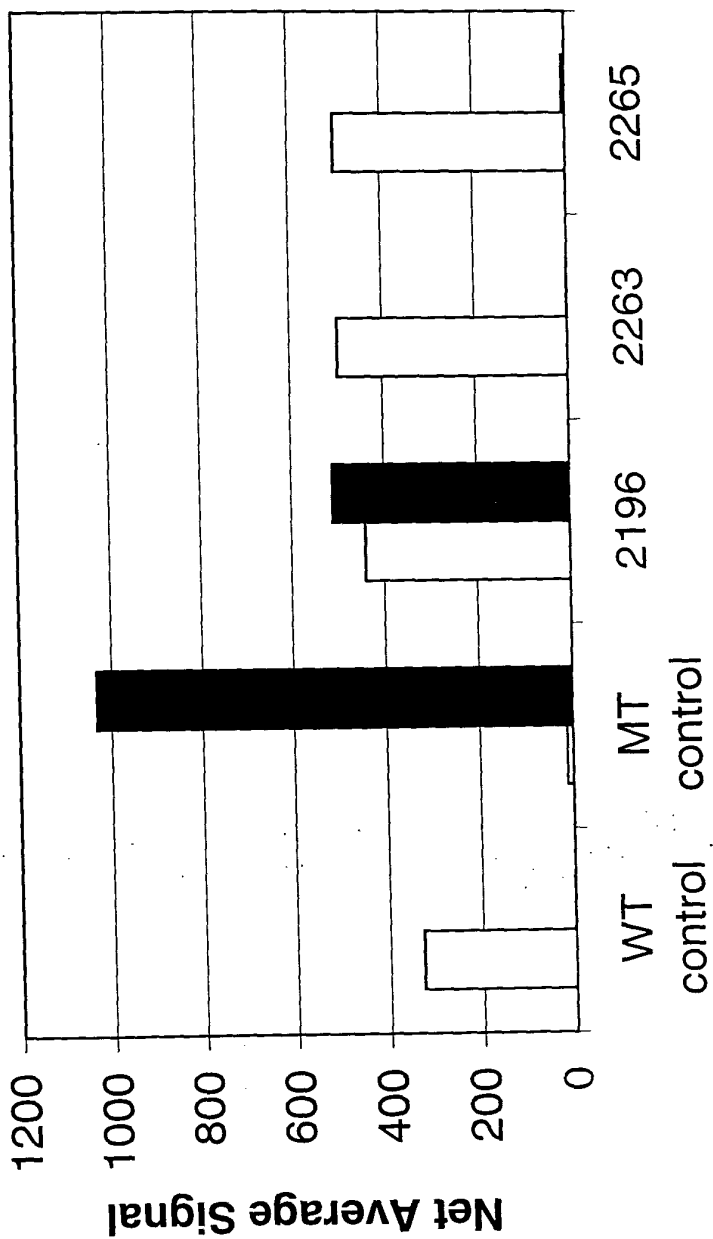
## FIGURE 119B

5'-AACGAGGCGCAC  
5'-TATGGTTCCCAATAAAAGTGACTCTCAGCT  
3'-TTGATACCAAGGGTTATTTTCACTGAGAGTCGTTCCGGAGTTACGAGGGTCA-5'

5'-AACGAGGCGCAC  
3'-NH<sub>2</sub>-TTTGCTCCCGTGGGAGCAGAGCCCT  
CCTCGTCTCGGT  
Cyt  
T

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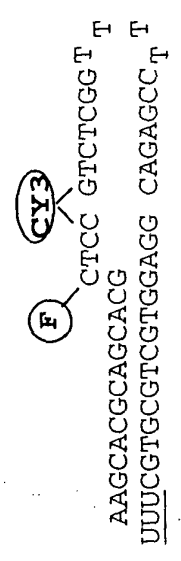
FIGURE 120



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# FIGURE 121A

5'-AAGCAGCAGCAC<sup>C</sup>GTACAACCCCTTTCTCTAGACAAA  
5'-AGATGCCCA<sup>T</sup>TTCTCCAGACCTCAGCCC  
3'-GTCTACGGGTAAAGAGGTCTGGAGTCGGCATGTTGGGAAAGAGATCTGAAGT-5'

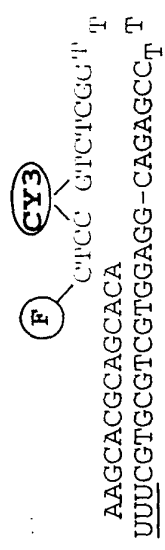




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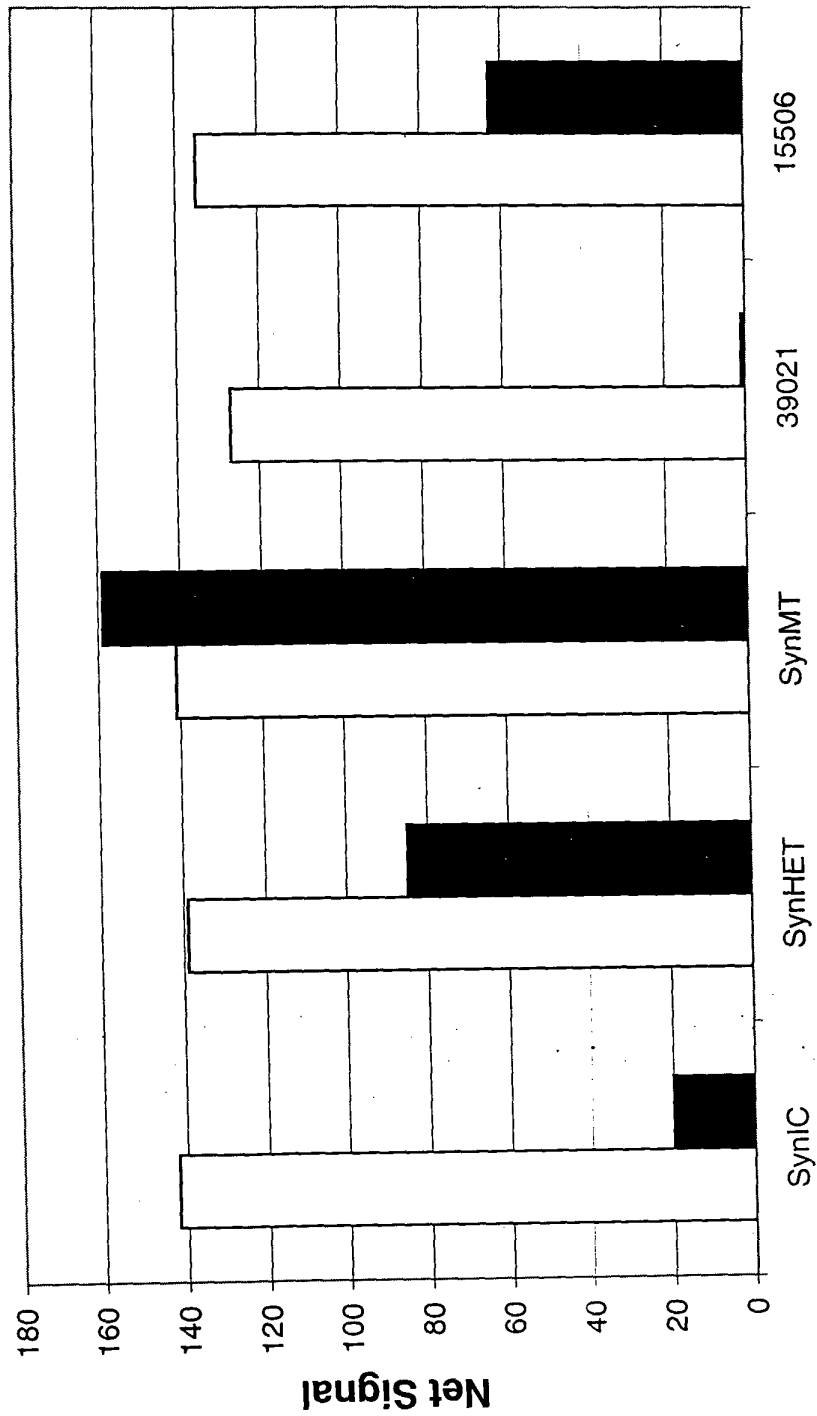
# FIGURE 121B

5'-AAGCAGGCAGCACAGGAACCCCTGTGACAT-3'  
5'-CCATCCAGGGAAGAGTGGCCGTGTT  
3'-GGTAGGTCCTTCTCACCGGACAATCCTTGGGACACTGTAAAGTTT-5'



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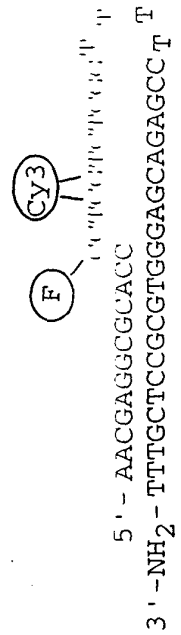
FIGURE 122



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FIGURE 123A

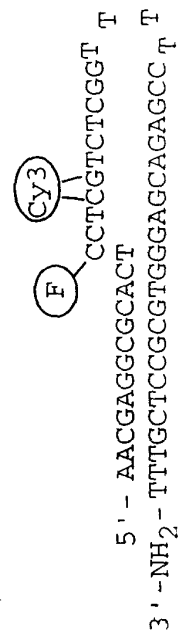
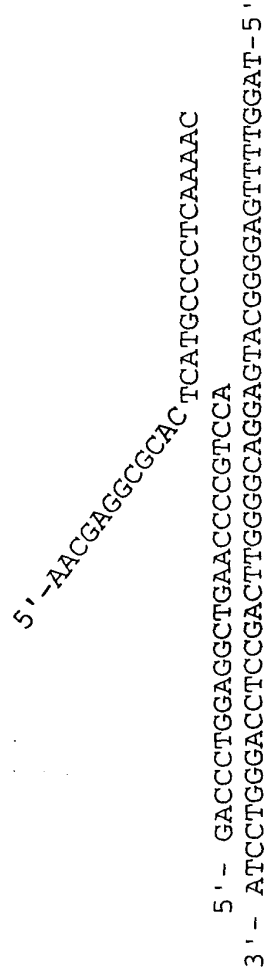
5'-AACGAGGCGCACCCATGCCCCCTCAAAAC  
5'-GACCCCTGGAGGCTGAACCCCGTCCA  
3'-ATCCTGGGACCTCCGACTTGGGCAGGGTACGGGAGTTTGGAT-5'



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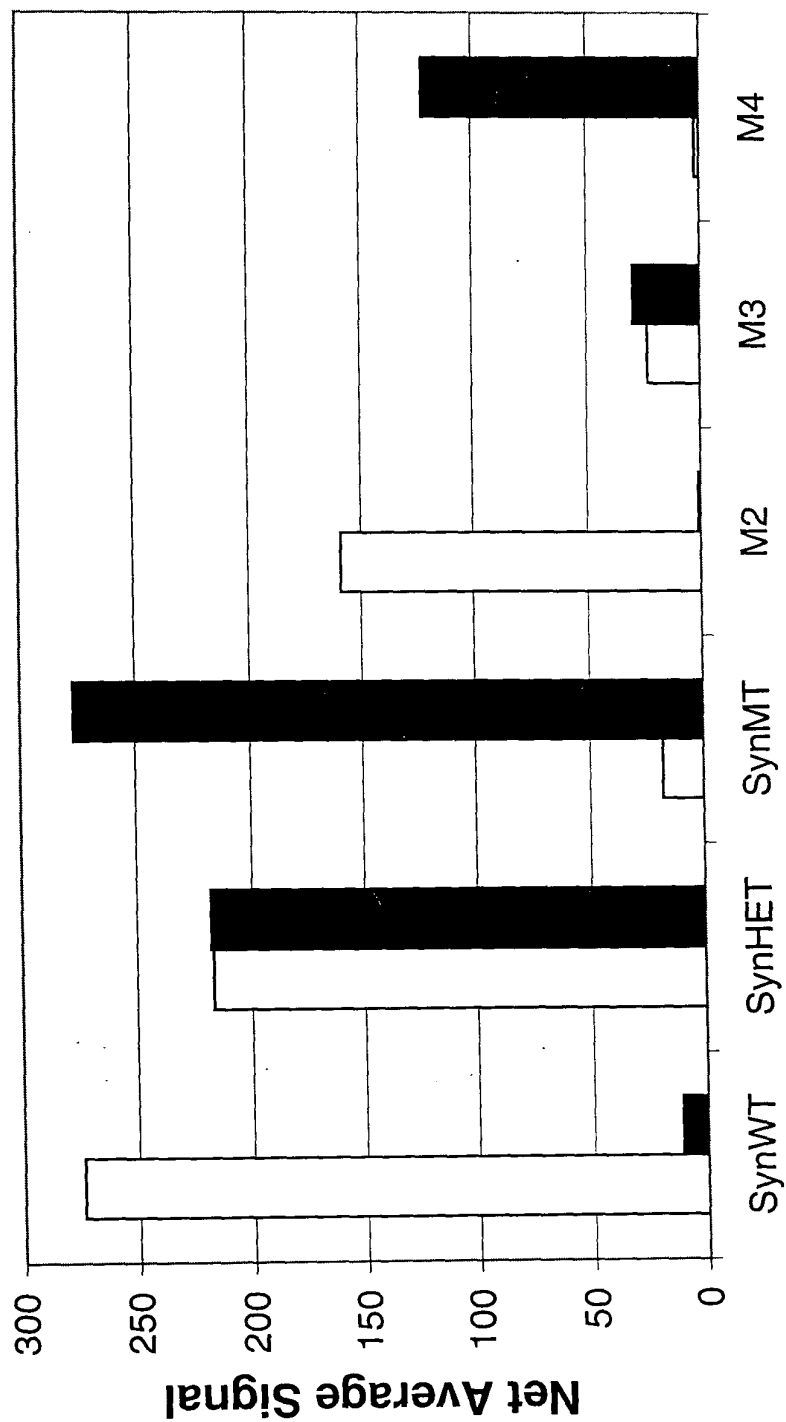
5'-AACGAGGCGCAC

FIGURE 123B



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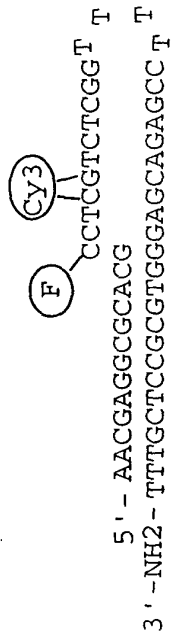
FIGURE 124



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# FIGURE 125A

5' - AACGAGGCGCAC GAGGAATACAGGTATTTGTC-NH3  
5' - TAATCTGTAAGAGCAGATCCCTGGACAGGCC  
3' - AGATTAGACATTCTCGTCTAGGGACCTGTCCGCTCCTTATGTCCATAAAACAGGAA-5'

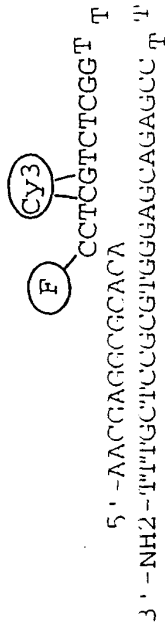


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Q U A T A T T A G A C A T T C T C G T C T A G G A C C T G T C C G T T C C T T A T G T C C A T A A A A C A G G A A - 5'

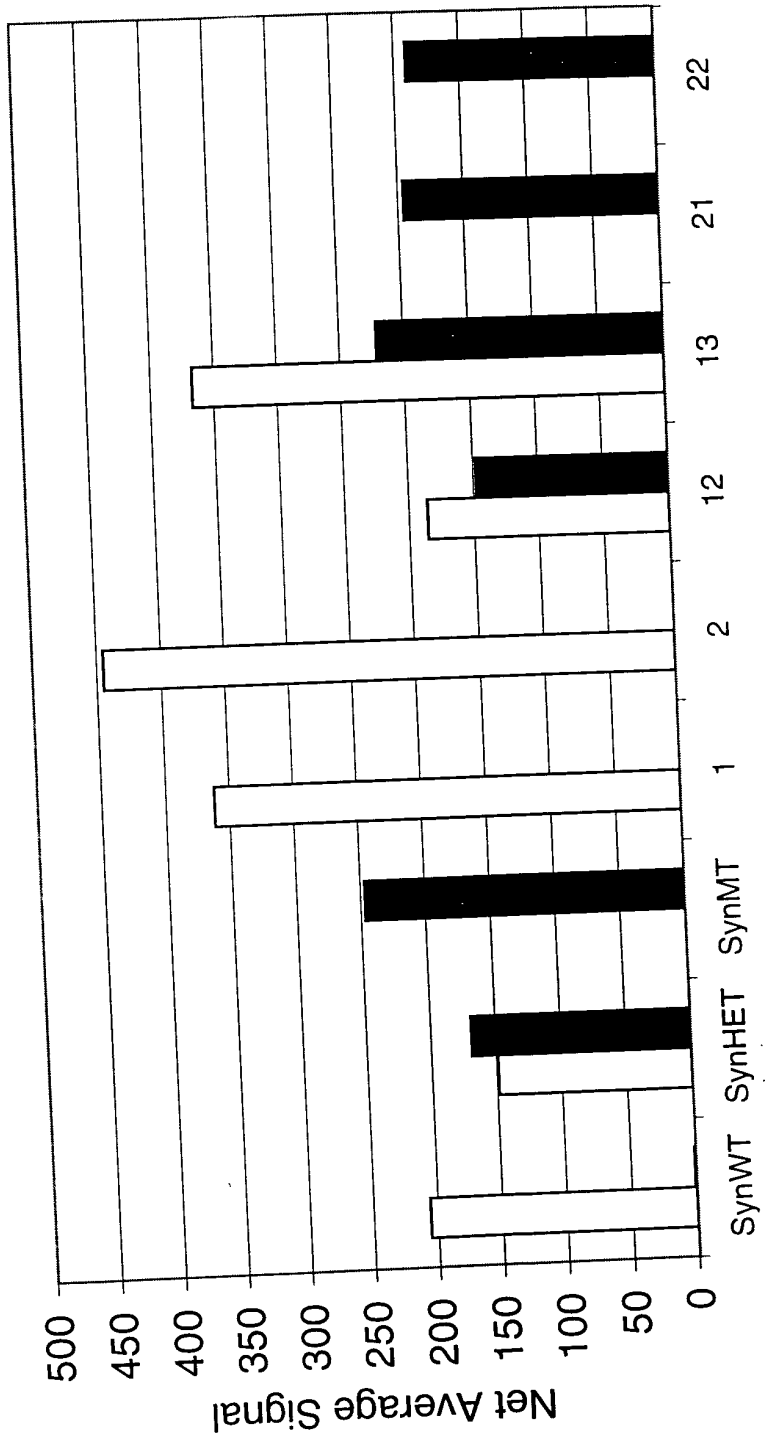
# FIGURE 125B

AACGAGGCGCAC AAGGAAATACAGGTATTTTGTGTC-NH3  
5' - TAATCTGTAAGAGCAGATCCCTGGACAGRCC  
3' - AGATTAGACATTTCTCGTCTAGGGACCTGTCCGTTCCCTTATGTCCATAAAACAGGAA - 5'



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FIGURE 126

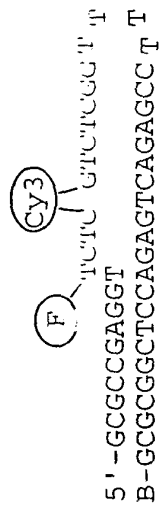




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## FIGURE 127A

5' - GCGCCGAGG TCTTGGGGTGGTTACAAG - NH<sub>2</sub> - 3'   
 5' - GGTAAGGTTGGCAAAAAGATAAC   
 CCATTCCAACCGTTTCTTATTAGAACCCCAATGTTTC - 5'



5' - CACTTGCTTCAGGACCATATTTCTCTC

## FIGURE 127B

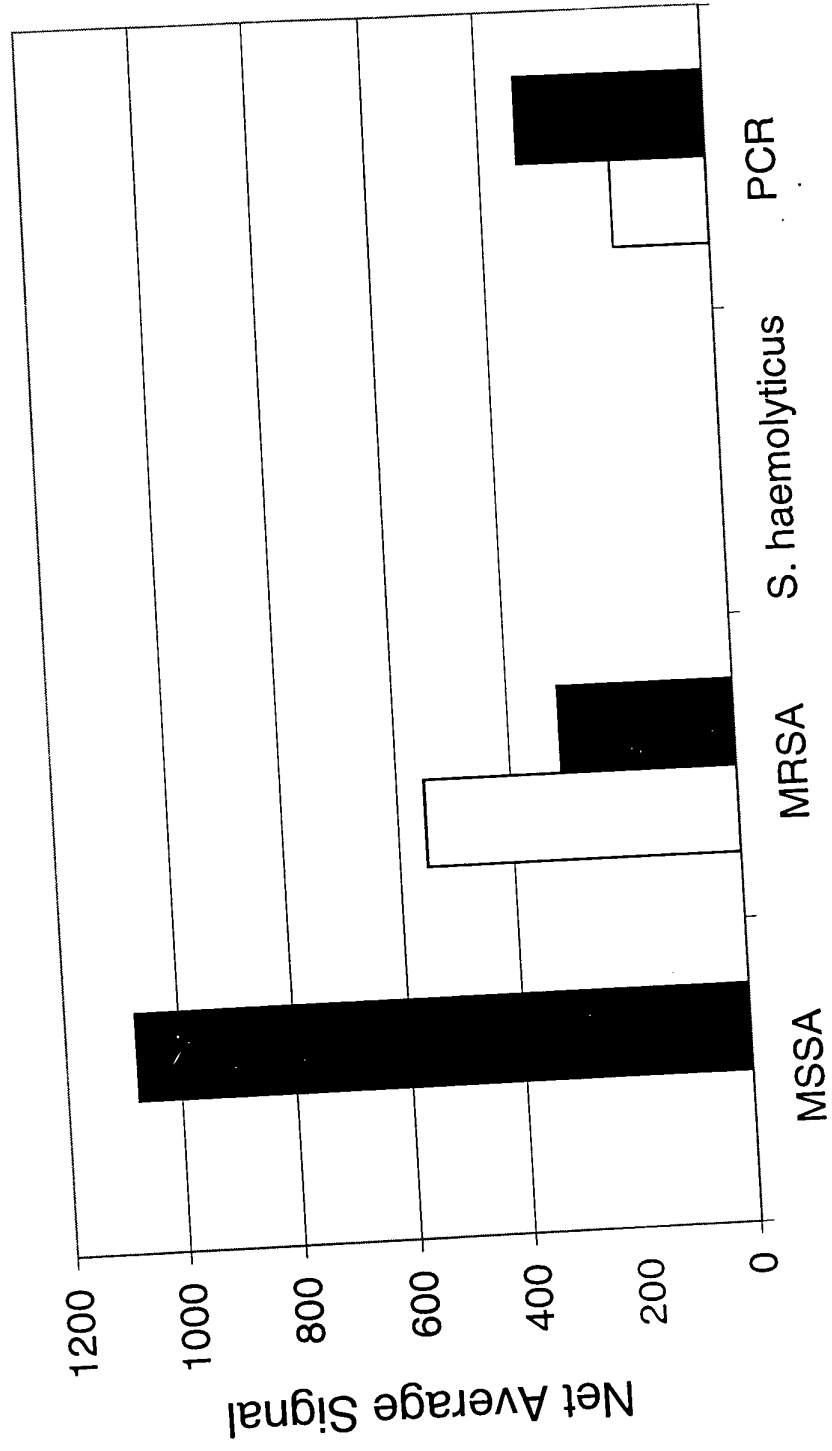
5' - CACTTGCTTCAGGACCATATTTCTCTC  
GTGAACGAAAGTCCTGGTATAAAGAGAGATGTGGAATAATCCACGAAACA - 5'

5' - CACTTGCTTCAGGACCATATTTCTCTC  
GTGAACGAAAGTCCTGGTATAAAGAGAGATGTGGAATAATCCACGAAACA - 5'

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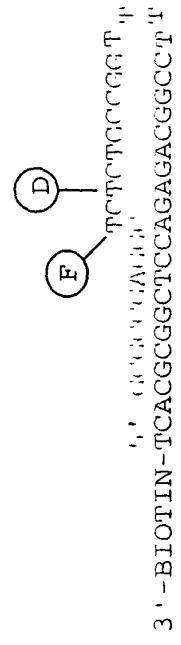
FIGURE 128



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# FIGURE 129

5' GCGCCGAGG CCGTTCTCTAGCGTGA-PO4 3'  
5' CCGAAGCAGCACAAAGCGGTGTGTACGA  
3' GGCTTCGTGCGTGTTCGCCACCCAGTGGCGGCAAGAGATCGCCACTGCGGACATATG 5'



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FIGURE 130

